



STIC SEARCH RESULTS

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library/CM1 - Circ. Desk



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STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 97246

TO: Nita M Minnifield
Location: 1/8a07 & 8e12
Art Unit: 1645
Tuesday, June 24, 2003

Case Serial Number: 002784

From: Edward Hart
Location: Biotech-Chem Library
CM1-6B02
Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Minnifield,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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97246

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Monday, June 23, 2003 1:16 PM
To: Minnifield, Nita; STIC-Biotech/ChemLib
Subject: RE: rush sequence search

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

From: Minnifield, Nita
Sent: Monday, June 23, 2003 12:47 PM
To: Chan, Christina
Subject: rush sequence search

Christina, please approve, 2 month amdt.

STIC

10/002784

Please do a commercial database search on SEQ ID NO: 16 and 27.

Please provide paper copy of the results.

Thanks,
Nita M. Minnifield
Art Unit 1645
Office CM1-8A07
Mailbox CM1-8E12
703-305-3394

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

6/23/03
ABSS02
2-AA

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WEST Search History

DATE: Tuesday, June 24, 2003

<u>Set Name</u> side by side	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u> result set
<i>DB=USPT,PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=YES; OP=ADJ</i>			
L11	l5 and pyrogenic adj5 exotoxin	18	L11
L10	L5 and pyrogenic	18	L10
L9	l7 and altered adj10 antigen receptor	4	L9
L8	L7 and altered adj10 class II	4	L8
L7	l5 and streptococc\$	77	L7
L6	L5 and streptococc?	13	L6
L5	bacterial adj5 superantigen	197	L5
L4	L3 and superantigen	3	L4
L3	l1 or L2	29	L3
L2	ulrich-robert-g.in.	3	L2
L1	ulrich-robert.in.	26	L1

END OF SEARCH HISTORY

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WEST

Generate Collection

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Search Results - Record(s) 1 through 4 of 4 returned.☐ 1. Document ID: US 20030036644 A1

L8: Entry 1 of 4

File: PGPB

Feb 20, 2003

PGPUB-DOCUMENT-NUMBER: 20030036644

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030036644 A1

TITLE: Bacterial superantigen vaccines

PUBLICATION-DATE: February 20, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Ulrich, Robert G.	Frederick	MD	US	

US-CL-CURRENT: 536/23.1; 536/23.7

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	NAC	Draw Data	Image
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☐ 2. Document ID: US 20030009015 A1

L8: Entry 2 of 4

File: PGPB

Jan 9, 2003

PGPUB-DOCUMENT-NUMBER: 20030009015

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030009015 A1

TITLE: BACTERIAL SUPERANTIGEN VACCINES

PUBLICATION-DATE: January 9, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
ULRICH, ROBERT G.	FREDERICK	MD	US	
OLSON, MARK A.	GAITHERSBURG	MD	US	
BAVARI, SINA	DILLSBURG	PA	US	

US-CL-CURRENT: 536/23.1; 424/184.1, 435/320.1

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments
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☐ 3. Document ID: US 6399332 B1

L8: Entry 3 of 4

File: USPT

Jun 4, 2002

US-PAT-NO: 6399332

DOCUMENT-IDENTIFIER: US 6399332 B1

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TITLE: Bacterial superantigen vaccines

DATE-ISSUED: June 4, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Ulrich; Robert G.	Frederick	MD		
Olson; Mark A.	Gaithersburg	MD		
Bavari; Sina	Dillsburg	PA		

US-CL-CURRENT: 435/69.3; 435/252.3, 435/252.33, 435/320.1, 435/325, 435/69.1,
435/71.1, 435/71.3, 536/23.1, 536/23.7

Full | Title | Caption | Front | Review | Classification | Date | Reference | Sequences | Attachments

Print | Draw Data | Image

☐ 4. Document ID: JP 2002522055 W WO 200009154 A1 AU 9889049 A EP 1105154 A1

L8: Entry 4 of 4

File: DWPI

Jul 23, 2002

DERWENT-ACC-NO: 2000-224177

DERWENT-WEEK: 200263

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TITLE: Nucleic acid encoding superantigen toxin useful as a vaccine and for
diagnosis of superantigen-associated bacterial infections

INVENTOR: BAVARI, S; OLSON, M A ; ULRICH, R G

PRIORITY-DATA: 1998WO-US16766 (August 13, 1998)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
JP 2002522055 W	July 23, 2002		103	C12N015/09
WO 200009154 A1	February 24, 2000	E	118	A61K039/00
AU 9889049 A	March 6, 2000		000	A61K039/00
EP 1105154 A1	June 13, 2001	E	000	A61K039/00

INT-CL (IPC): A61 K 39/00; A61 K 39/02; A61 K 39/085; A61 K 39/09; A61 K 39/44; A61
P 31/00; A61 P 35/00; A61 P 37/04; C07 K 14/00; C07 K 14/31; C12 N 1/20; C12 N 1/21;
C12 N 15/00; C12 N 15/09; C12 N 15/63; C12 P 21/00; C12 P 21/02; G01 N 33/53; G01 N
33/569

Full | Title | Caption | Front | Review | Classification | Date | Reference | Sequences | Attachments

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Term	Documents
ALTERED	229335
ALTEREDS	0
CLASS	289019
CLASSES	110796
II	1492271
IIS	1903
(7 AND (ALTERED ADJ10 CLASS ADJ II)).USPT,PGPB,JPAB,EPAB,DWPI,TDBD.	4
(L7 AND ALTERED ADJ10 CLASS II).USPT,PGPB,JPAB,EPAB,DWPI,TDBD.	4

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Search Results - Record(s) 1 through 18 of 18 returned.

☐ 1. Document ID: US 20030092894 A1

L11: Entry 1 of 18

File: PGPB

May 15, 2003

PGPUB-DOCUMENT-NUMBER: 20030092894

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030092894 A1

TITLE: Modified chimeric superantigens and their use

PUBLICATION-DATE: May 15, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Antonsson, Per	Lund		SE	
Bjork, Per	Helsingborg		SE	
Dohlsten, Mikael	Lund		SE	
Kalland, Terje	Arese		IT	
Hansson, Johan	Lund		SE	
Forsberg, Goran	Lund		SE	
Abrahmsen, Lars	Bromma		SE	

US-CL-CURRENT: 530/388.1; 435/7.23, 530/388.8[Full](#) | [Title](#) | [Caption](#) | [Front](#) | [Review](#) | [Classification](#) | [Date](#) | [Reference](#) | [Sequences](#) | [Attachments](#)[Image](#) | [Draw Page](#) | [Image](#)☐ 2. Document ID: US 20030036644 A1

L11: Entry 2 of 18

File: PGPB

Feb 20, 2003

PGPUB-DOCUMENT-NUMBER: 20030036644

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20030036644 A1

TITLE: Bacterial superantigen vaccines

PUBLICATION-DATE: February 20, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Ulrich, Robert G.	Frederick	MD	US	

US-CL-CURRENT: 536/23.1; 536/23.7[Full](#) | [Title](#) | [Caption](#) | [Front](#) | [Review](#) | [Classification](#) | [Date](#) | [Reference](#) | [Sequences](#) | [Attachments](#)[Image](#) | [Draw Page](#) | [Image](#)☐ 3. Document ID: US 20030009015 A1

2 PAGE BLANK (USPTO)

L11: Entry 3 of 18

File: PGPB

Jan 9, 2003

PGPUB-DOCUMENT-NUMBER: 20030009015
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20030009015 A1

TITLE: BACTERIAL SUPERANTIGEN VACCINES

PUBLICATION-DATE: January 9, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
ULRICH, ROBERT G.	FREDERICK	MD	US	
OLSON, MARK A.	GAITHERSBURG	MD	US	
BAVARI, SINA	DILLSBURG	PA	US	

US-CL-CURRENT: 536/23.1; 424/184.1, 435/320.1

Full	Title	Citation	Front	Revised	Classification	Date	Reference	Sequences	Attachments
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Table	Table Desc	Image
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☐ 4. Document ID: US 20020197234 A1

L11: Entry 4 of 18

File: PGPB

Dec 26, 2002

PGPUB-DOCUMENT-NUMBER: 20020197234
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020197234 A1

TITLE: Immunologic activities of rhesus cytomegalovirus encoded IL-10 and human cytomegalovirus encoded IL-10

PUBLICATION-DATE: December 26, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Schall, Thomas J.	Menlo Park	CA	US	
Penfold, Mark	Mountain View	CA	US	
Spencer, Juliet	Foster City	CA	US	

US-CL-CURRENT: 424/85.2; 424/93.7, 435/372

Full	Title	Citation	Front	Revised	Classification	Date	Reference	Sequences	Attachments
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Table	Table Desc	Image
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☐ 5. Document ID: US 6514498 B1

L11: Entry 5 of 18

File: USPT

Feb 4, 2003

US-PAT-NO: 6514498
DOCUMENT-IDENTIFIER: US 6514498 B1

TITLE: Modified/chimeric superantigens and their use

DATE-ISSUED: February 4, 2003

INVENTOR-INFORMATION:

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NAME	CITY	STATE	ZIP CODE	COUNTRY
Antonsson; Per	Lund			SE
Bjork; Per	Helsingborg			SE
Dohlsten; Mikael	Lund			SE
Hansson; Johan	Lund			SE
Forsberg; Goran	Lund			SE
Abrahmsen; Lars	Bromma			SE
Kalland; Terje	Arese			IT

US-CL-CURRENT: 424/178.1; 424/182.1, 424/184.1, 424/185.1, 424/190.1, 424/192.1,
424/194.1

Full Title Edition Front Review Classification Date Reference Sequences Attachments

Find Draw Desc Image

☐ 6. Document ID: US 6447777 B1

L11: Entry 6 of 18

File: USPT

Sep 10, 2002

US-PAT-NO: 6447777

DOCUMENT-IDENTIFIER: US 6447777 B1

TITLE: Polymerized staphylococcal protein a for treatment of diseases

DATE-ISSUED: September 10, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Terman; David Stephen	Pebble Beach	CA		
Reiser; Raoul F.	Sarasota	FL		

US-CL-CURRENT: 424/184.1; 424/236.1, 424/237.1, 424/243.1, 424/280.1, 514/12,
514/18, 530/350, 530/387.1

Full Title Edition Front Review Classification Date Reference Sequences Attachments

Find Draw Desc Image

☐ 7. Document ID: US 6399332 B1

L11: Entry 7 of 18

File: USPT

Jun 4, 2002

US-PAT-NO: 6399332

DOCUMENT-IDENTIFIER: US 6399332 B1

TITLE: Bacterial superantigen vaccines

DATE-ISSUED: June 4, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Ulrich; Robert G.	Frederick	MD		
Olson; Mark A.	Gaithersburg	MD		
Bavari; Sina	Dillsburg	PA		

US-CL-CURRENT: 435/69.3; 435/252.3, 435/252.33, 435/320.1, 435/325, 435/69.1,
435/71.1, 435/71.3, 536/23.1, 536/23.7

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Full Title Creation Front Review Classification Date Reference Sequences Attachments

Form Draw Desc Image

☐ 8. Document ID: US 6340461 B1

L11: Entry 8 of 18

File: USPT

Jan 22, 2002

US-PAT-NO: 6340461

DOCUMENT-IDENTIFIER: US 6340461 B1

TITLE: Superantigen based methods and compositions for treatment of diseases

DATE-ISSUED: January 22, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Terman; David Stephen	Pebble Beach	CA	93953	

US-CL-CURRENT: 424/193.1; 424/192.1, 424/194.1, 424/277.1, 424/278.1, 424/280.1,
424/282.1, 435/68.1, 435/69.1, 435/69.3, 435/69.7

Full Title Creation Front Review Classification Date Reference Sequences Attachments

Form Draw Desc Image

☐ 9. Document ID: US 6338845 B1

L11: Entry 9 of 18

File: USPT

Jan 15, 2002

US-PAT-NO: 6338845

DOCUMENT-IDENTIFIER: US 6338845 B1

TITLE: Tumor killing effects of enterotoxins, superantigens, and related compounds

DATE-ISSUED: January 15, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Terman; David S.	Pebble Beach	CA	93953	

US-CL-CURRENT: 424/93.1; 424/93.2, 424/93.21, 424/93.7, 424/93.71, 435/372,
435/372.1, 435/372.2, 435/372.3

Full Title Creation Front Review Classification Date Reference Sequences Attachments

Form Draw Desc Image

☐ 10. Document ID: US 6251385 B1

L11: Entry 10 of 18

File: USPT

Jun 26, 2001

US-PAT-NO: 6251385

DOCUMENT-IDENTIFIER: US 6251385 B1

TITLE: Method of cancer treatment

DATE-ISSUED: June 26, 2001

INVENTOR-INFORMATION:

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NAME	CITY	STATE	ZIP CODE	COUNTRY
Terman; David S.	Pebble Beach	CA	93953	

US-CL-CURRENT: 424/93.7; 424/184.1, 424/236.1, 424/237.1, 424/277.1, 424/93.1,
424/93.2, 424/93.71, 435/325

Full Title Caption Print Review Classification Date Reference Sequences Attachments

Full Draw Desc Image

☐ 11. Document ID: US 6221351 B1

L11: Entry 11 of 18

File: USPT

Apr 24, 2001

US-PAT-NO: 6221351

DOCUMENT-IDENTIFIER: US 6221351 B1

TITLE: Tumor killing effects of enterotoxins, superantigens, and related compounds

DATE-ISSUED: April 24, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Terman; David S.	Pebble Beach	CA	93953	

US-CL-CURRENT: 424/93.71; 424/93.1, 424/93.2, 424/93.21, 424/93.7, 435/69.3, 514/44,
530/395

Full Title Caption Print Review Classification Date Reference Sequences Attachments

Full Draw Desc Image

☐ 12. Document ID: US 6126945 A

L11: Entry 12 of 18

File: USPT

Oct 3, 2000

US-PAT-NO: 6126945

DOCUMENT-IDENTIFIER: US 6126945 A

TITLE: Tumor killing effects of enterotoxins, superantigens, and related compounds

DATE-ISSUED: October 3, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Terman; David S.	Pebble Beach	CA		
Stone; Jay L.	Aptos	CA		

US-CL-CURRENT: 424/237.1; 424/236.1, 424/243.1, 424/244.1, 435/69.1, 435/69.3,
514/12, 514/8

Full Title Caption Print Review Classification Date Reference Sequences Attachments

Full Draw Desc Image

☐ 13. Document ID: US 6075119 A

L11: Entry 13 of 18

File: USPT

Jun 13, 2000

US-PAT-NO: 6075119

DOCUMENT-IDENTIFIER: US 6075119 A

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TITLE: Peptides useful for reducing symptoms of toxic shock syndrome

DATE-ISSUED: June 13, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Bannan; Jason D.	Thompson Station	TN		
Zabriskie; John B.	New York	NY		

US-CL-CURRENT: 530/300; 424/130.1, 424/185.1, 424/192.1, 424/243.1, 424/244.1,
530/324, 530/325, 530/326, 530/327, 530/328, 530/333, 530/350

Full Title Creation Front Review Classification Date Reference Sequences Attachments

Page Origin Date Image

☐ 14. Document ID: US 5872233 A

L11: Entry 14 of 18

File: USPT

Feb 16, 1999

US-PAT-NO: 5872233

DOCUMENT-IDENTIFIER: US 5872233 A

TITLE: Mycoplasma arthritidis T-cell mitogen

DATE-ISSUED: February 16, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Cole; Barry C.	Sandy	UT		
Atkin; Curtis L.	Salt Lake City	UT		
Oliphant; Arnold R.	Johnston	IA		
Pole; Ann	Salt Lake City	UT		

US-CL-CURRENT: 536/23.7; 435/69.1, 436/86, 530/300, 530/324, 530/350, 536/22.1,
536/23.1, 536/25.3

Full Title Creation Front Review Classification Date Reference Sequences Attachments

Page Origin Date Image

☐ 15. Document ID: US 5795974 A

L11: Entry 15 of 18

File: USPT

Aug 18, 1998

US-PAT-NO: 5795974

DOCUMENT-IDENTIFIER: US 5795974 A

TITLE: Mycoplasma arthritidis superantigen

DATE-ISSUED: August 18, 1998

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Cole; Barry C.	Sandy	UT		
Atkin; Curtis L.	Holladay	UT		
Knudtson; Kevin L.	Salt Lake City	UT		

US-CL-CURRENT: 536/23.7; 435/5, 435/7.2

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Full	Title	Caption	Print	Review	Classification	Date	Reference	Sequences	Attachments
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☐ 16. Document ID: US 5728388 A

L11: Entry 16 of 18

File: USPT

Mar 17, 1998

US-PAT-NO: 5728388

DOCUMENT-IDENTIFIER: US 5728388 A

TITLE: Method of cancer treatment

DATE-ISSUED: March 17, 1998

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Terman; David S.	Pebble Beach	CA	93953	

US-CL-CURRENT: 424/237.1; 424/236.1

Full	Title	Caption	Print	Review	Classification	Date	Reference	Sequences	Attachments
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Full	Draw Desc	Image
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☐ 17. Document ID: US 5639869 A

L11: Entry 17 of 18

File: USPT

Jun 17, 1997

US-PAT-NO: 5639869

DOCUMENT-IDENTIFIER: US 5639869 A

TITLE: Mycoplasma arthritidis T-cell mitogen

DATE-ISSUED: June 17, 1997

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Cole; Barry C.	Sandy	UT		
Atkin; Curtis L.	Salt Lake City	UT		
Oliphant; Arnold R.	Johnston	IA		
Pole; Ann	Salt Lake City	UT		

US-CL-CURRENT: 536/23.7; 424/264.1, 530/326, 530/350, 530/825

Full	Title	Caption	Print	Review	Classification	Date	Reference	Sequences	Attachments
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Full	Draw Desc	Image
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☐ 18. Document ID: US 6447777 B1 WO 9736614 A1 AU 9724293 A

L11: Entry 18 of 18

File: DWPI

Sep 10, 2002

DERWENT-ACC-NO: 1997-549326

DERWENT-WEEK: 200263

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TITLE: Use of crosslinked Staphylococcal protein A - for treating auto-immune diseases, transplant rejection neoplastic diseases or infectious disease such as HIV infection

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INVENTOR: REISER, R F; TERMAN, D S

PRIORITY-DATA: 1996US-024802P (March 29, 1996), 1997US-0828951 (March 28, 1997)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
US 6447777 B1	September 10, 2002		000	A61K039/02
WO 9736614 A1	October 9, 1997	E	100	A61K039/09
AU 9724293 A	October 22, 1997		000	A61K039/09

INT-CL (IPC): A61 K 38/00; A61 K 39/02; A61 K 39/04; A61 K 39/085; A61 K 39/09; A61 K 45/00; A61 K 47/04; C07 K 1/00; C07 K 14/24; C07 K 14/315; C07 K 14/35; C07 K 17/02; C07 K 17/06; C07 K 17/14

[Full](#) [Title](#) [Citation](#) [Front](#) [Review](#) [Classification](#) [Date](#) [References](#) [Sequences](#) [Attachments](#)[Image](#) [Image Data](#) [Image](#)[Generate Collection](#)[Print](#)

Term	Documents
PYROGENIC	7502
PYROGENICS	13
EXOTOXIN	4369
EXOTOXINS	847
(5 AND (PYROGENIC ADJ5 EXOTOXIN)).USPT,PGPB,JPAB,EPAB,DWPI,TDBD.	18
(L5 AND PYROGENIC ADJ5 EXOTOXIN).USPT,PGPB,JPAB,EPAB,DWPI,TDBD.	18

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 16:06:15 ; Search time 36.6551 seconds

(without alignments)
912.449 Million cell updates/sec

Title: US-10-002-784a-16

Perfect score: 1332

Sequence: 1 MNNKVLKKWFFVLYTFL.....KDNETLDSNTSQIEVYLTTK 251

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_101002:*

- 1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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- 18: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1332	100.0	251	21	AAV70109
2	1332	100.0	251	23	ABB79508
3	1308	98.9	251	18	AAW12097
4	1308	98.9	251	19	AAW59780
5	1305	98.7	251	18	AAW12154
6	1304	98.6	251	18	AAW12146
7	1303	98.6	251	18	AAW12150
8	1303	98.6	251	18	AAW12147
9	1299	98.3	251	18	AAW12148
10	1298	98.2	251	18	AAW12151

11	1298	98.2	251	18	AAW12152	Streptococcus pyog
12	1298	98.2	251	18	AAW12153	Streptococcus pyog
13	1293	97.8	251	18	AAW12149	Streptococcus pyog
14	1288.5	97.5	250	18	AAW12145	Streptococcus pyog
15	1288	97.4	251	19	AAW59798	Amino acid sequenc
16	1286	97.3	251	19	AAW59781	Amino acid sequenc
17	1170	88.5	221	22	AAW67344	Streptococcus pyro
18	1164	88.0	221	12	AAW13309	Streptococcal pyro
19	1164	88.0	221	14	AAW45017	Streptococcal ent
20	1164	88.0	221	23	ABB76240	Streptococcus pyo
21	1164	88.0	225	18	AAW06737	Streptococcus ent
22	576	43.6	239	19	AAW64647	Synthetic SEB prot
23	575	43.5	266	21	AAV92319	Plant-optimized mu
24	574	43.4	239	22	AAW67341	Streptococcus ent
25	567.5	42.9	266	23	ABB79503	Streptococcal ent
26	565.5	42.8	266	21	AAV54464	Amino acid sequenc
27	563	42.6	239	23	ABB79505	Streptococcal ent
28	563	42.6	240	21	AAV54465	Mutant Streptococ
29	562	42.5	239	23	ABB76237	Streptococcus aur
30	561	42.4	239	12	AAW13206	Streptococcal ent
31	561	42.4	239	14	AAW45014	Streptococcal ent
32	558.5	42.2	266	23	ABB79504	Streptococcal ent
33	558	42.2	239	21	AAV70106	Mutant Streptococ
34	553	41.8	266	21	AAV70108	Streptococcal ent
35	553	41.8	266	23	ABB79507	Streptococcal SEC
36	549	41.5	265	21	AAV70104	Streptococcal ent
37	547	41.4	239	20	AAW06254	Streptococcal gro
38	546	41.3	238	23	ABB76239	Streptococcus aur
39	545	41.2	238	14	AAW45016	Streptococcal ent
40	545	41.2	238	22	AAW67343	Streptococcus aur
41	544	41.1	239	12	AAW13207	Streptococcal ent
42	544	41.1	239	14	AAW45015	Streptococcal ent
43	544	41.1	239	20	AAW06251	Streptococcal gro
44	544	41.1	239	22	AAW67342	Streptococcus aur
45	544	41.1	239	23	ABB76238	Streptococcus aur

ALIGNMENTS

RESULT 1	AAV70109	standard; Protein; 251 AA.
ID	AAV70109	
XX	AAV70109;	
AC	AAV70109;	
XX		
DT	05-JUN-2000 (first entry)	
XX		
DE	Streptococcal pyrogenic exotoxin A (SPE-A).	
XX		
KW	Superantigen toxin; SAg; Streptococcal pyrogenic exotoxin A; SPE-A;	
KW	antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;	
KW	cytotoxic; antibody; staphylococcal/streptococcal toxin; toxoid; SPEA2;	
KW	diagnosis; treatment; superantigen-associated bacterial infection.	
XX		
OS	Streptococcus sp.	
XX		
PN	WO200009154-A1.	
XX		
PD	24-FEB-2000.	
XX		
PF	13-AUG-1998; 98WO-US16766.	
XX		
PR	13-AUG-1998; 98WO-US16766.	
XX		
PA	(REED-) REED ARMY INST RES WALTER.	
XX		
PI	Ulrich RG, Olson MA, Bavari S;	
XX		
DR	WPI, 2000-224177/19.	
XX		
DR	N-PSDB; AA251112.	
XX		
PT	Nucleic acid encoding superantigen toxin useful as a vaccine and for	

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PT diagnosis of superantigen-associated bacterial infections -
xx Example 12: Page 94-95; 110pp; English.
xx
xx The present amino acid sequence is the Streptococcal pyrogenic
CC exotoxin A (SPE-A), a bacterial superantigen toxin (Sag), used for the
CC formulation of SPE-A vaccine SPEA42. The coding region of this Sag toxin
CC is altered by site directed mutagenesis, introducing 142R mutation, that
CC results in disruption of binding of the toxin to both the MHC class II
CC or T-cell antigen receptor. SPE-A has antibacterial and cytostatic
CC activity. This sequence is useful for the production of SPE-A vaccines
CC and specific antibodies. This vaccine overcomes the disadvantages of the
CC chemically inactivated toxoids and is designed to protect individuals
CC against one or several related streptococcal and streptococcal toxins.
CC It is used for the diagnosis and treatment or amelioration of
CC superantigen-associated bacterial infections.
xx
xx Sequence 251 AA:
xx
xx Query Match 100.0%; Score 1322; DB 21; Length 251;
xx Best Local Similarity 100.0%; Pred. No. 4,5e-111;
xx Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
xx
xx QY 1 MNNKKVLLKKVFFVLTFLGTTISQEVFAQDDPPDSQLHRSLSLVKNLQNTIFYLEGDPV 60
xx Db 1 MNNKKVLLKKVFFVLTFLGTTISQEVFAQDDPPDSQLHRSLSLVKNLQNTIFYLEGDPV 60
xx QY 61 THENKSVDOILSRHDLIYNVSGPNVDKLTTELKNQEMATLFPDKRWVDYGYEYHALCYLC 120
xx Db 61 THENKSVDOILSRHDLIYNVSGPNVDKLTTELKNQEMATLFPDKRWVDYGYEYHALCYLC 120
xx QY 121 ENAERSACIYGGVTNHGEKNHLEIPRKIVKVSIDGISOGLSPDIETNNKRWTAQELDYKVR 180
xx Db 121 ENAERSACIYGGVTNHGEKNHLEIPRKIVKVSIDGISOGLSPDIETNNKRWTAQELDYKVR 180
xx QY 181 KYLDNRKQLYTNGSPKETEYTKFIPKKNKESFMPDFPEPEPTOSKYLMTYKDNFTLDSN 240
xx Db 181 KYLDNRKQLYTNGSPKETEYTKFIPKKNKESFMPDFPEPEPTOSKYLMTYKDNFTLDSN 240
xx QY 241 TSOIEVYLLTK 251
xx Db 241 TSOIEVYLLTK 251
xx
xx RESULT 2
xx ABB79508
xx ID ABB79508 standard; Protein: 251 AA.
xx AC ABB79508;
xx XX
xx DT 23-SEP-2002 (first entry)
xx DE
xx KM Streptococcal pyrogenic exotoxin A vaccine SPEA42.
xx KN exotoxin A; SPEA; SPEA42; superantigen; antigen; toxin; vaccine;
xx OS attenuation; mutant; mutelin.
xx OS Streptococcus pyogenes.
xx OS Synthetic.
xx OS
xx PN US6399332-B1.
xx PD 04-JUN-2002.
xx PE 01-SEP-1998; 98US-0144776.
xx PR 25-JUN-1997; 97US-0882431.
xx PA (USSA ) US SEC OF ARMY.
xx PI Ulrich RG, Olson MA, Bavari S;
xx WPI; 2002-546281/58.

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DR	N-PSDB, ABR84229.
XX	Novel isolated and purified superantigen toxin DNA fragment which has
PT	been genetically altered, useful for producing vaccine for treatment of
PT	superantigen toxin-associated bacterial diseases
XX	
PS	Disclosure; Column 63-65; 46pp. English.
XX	
CC	The present sequence is the protein sequence of Streptococcus
CC	pyogenes vaccine SPB42. The vaccine differs from the native SPBA
CC	sequence by substitution of the Leu-42 residue by Arg. This
CC	mutation is expected to disrupt contact between the toxin and the
CC	HLA-DR receptor, reducing DRI binding. SPB42 can be expressed as
CC	a recombinant protein in Escherichia coli as a secreted protein or
CC	as a cytoplasmic product. No indicators of toxicity have been
CC	detected for the purified recombinant protein, and vaccine studies
CC	demonstrate that SPB42 is highly antigenic, inducing protective
CC	immunity in a mouse animal model. The attenuated superantigen can
CC	be used to protect against superantigen toxin infections. Methods of
CC	producing and using altered superantigen toxins as vaccines, and in
CC	diagnosis and therapy, are provided by the invention. A multivalent
CC	vaccine consisting of altered superantigen toxins from SEA, SEB,
CC	SEC1, TSST-1 and SPBA is predicted to provide protective immunity
CC	against the majority of bacterial superantigen toxins.
XX	
SO	Sequence 251 AA:
Query Match	100.0%; Score 132; DB 23; Length 251;
Best Local Similarity	100.0%; Pred. No. 4,56-111;
Matches	251; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 MNNKRVLKKWFEVLVTLGLTISQEVPAQDDPPSOLHNSLVKLNQNIYFLYEGDPV 60
DB	1 MNNKRVLKKWFEVLVTLGLTISQEVPAQDDPPSOLHNSLVKLNQNIYFLYEGDPV 60
OY	THENVKSVDO.LRSHDLINYNAGSPNVDKLTTELKNQEMATLFDKRVNDYGVGYHLCTYC 120
DB	61 THENKSVDO.LRSHDLINYNAGSPNVDKLTTELKNQEMATLFDKRVNDYGVGYHLCTYC 120
OY	121 ENERSACIYGVVTNHEGNNHLEIPKRIYKVSIDSIGSLSPDIETNNKRVTAQOELDYKVR 180
DB	121 ENERSACIYGVVTNHEGNNHLEIPKRIYKVSIDSIGSLSPDIETNNKRVTAQOELDYKVR 180
OY	181 KYLDNRKOLYNGSPKYEFGYIKFLPKKESFMPFPPEPTOSKYLMIYKDNFTLSN 240
DB	181 KYLDNRKOLYNGSPKYEFGYIKFLPKKESFMPFPPEPTOSKYLMIYKDNFTLSN 240
OY	241 TSQIEVYLVTK 251
DB	241 TSQIEVYLVTK 251
RESULT 3	
AAWI2097	AAWI2097 standard; Protein: 251 AA.
XX	AAWI2097:
XX	04-NOV-1997 (first entry)
DE	Streptococcus pyogenes Streptococcal toxin A.
XX	
KW	Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
KW	vaccine; protection; treatment; cancer; neutralising antibody;
KW	streptococcal toxic shock syndrome; STSS; symptom; amelioration;
KW	fever; hypotension; group A streptococcal infection; myositis;
XX	fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
OS	Streptococcus pyogenes.
XX	
XX	Key
XX	Location/Qualifiers
XX	1..30
XX	Peptide
XX	/label=sig_peptide
XX	FT

FT Peptide 31.251
 /label= mat_peptide
 PN MO9640930-A1.
 XX 19-DEC-1996.
 PD
 XX 07-JUN-1996; 96WO-US10252.
 PF
 XX 07-JUN-1995; 95US-0480261.
 PR
 PA (MINU) UNIV MINNESOTA.
 PI Ohlendorf D, Roggiani M, Schlievert PM, Stoehr J;
 DR WPI: 1997-099936/09.
 DR N-PSDB; AAW12097.
 XX
 XX Mutant SPE-A toxin with at least one amino acid change is
 PT substantially non-lethal - used in vaccine composition for
 PT treatment of cancer and streptococcal toxic shock syndrome etc.
 PS Disclosure; Pages 77-79; 102pp; English.
 XX
 XX The present sequence is Streptococcus pyogenes Streptococcal
 CC toxin A (SPE-A), from which a non-lethal mutant SPE-A, comprising
 CC at least 1 amino acid change, can be derived. The mutant SPE-A can
 CC be used to produce vaccines to protect animals against wild type
 CC SPE-A and to treat cancer and streptococcal toxic shock syndrome
 CC (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be
 CC produced, which may be used to ameliorate STSS symptoms, e.g.
 CC fever, hypotension, group A streptococcal infection, abscesses,
 CC fasciitis and liver damage. The neutralising Ab is preferably
 CC administered in conjunction with antibiotic therapy. The mutant
 CC SPE-A is especially useful for treating T cell lymphomas, and
 CC ovarian and uterine cancer. It is thought that mutant SPE-A can be
 CC selectively toxic to T cell lymphoma cells.
 XX
 SQ Sequence 251 AA:
 Query Match 98.9%; Score 1308; DB 18; Length 251;
 Best Local Similarity 99.2%; Pred. No. 8.3e-110;
 Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 MENNKKVYKRMVFVLTFLGLTISOEYFAQDDPSQLHRSSLYKNLONIFYLYEGDPV 60
 DB 1 MENNKKVYKRMVFVLTFLGLTISOEYFAQDDPSQLHRSSLYKNLONIFYLYEGDPV 60
 OY 61 THENKSVYDQLRSHDLIYVNSGPNYDKLTTELKNOEMATLFDKKNVDIYGEYHLCYLC 120
 DB 61 THENKSVYDQLRSHDLIYVNSGPNYDKLTTELKNOEMATLFDKKNVDIYGEYHLCYLC 120
 OY 121 ENAERSACITGGVTNHEGHNLEIPKTIYVNSIDGISOISFDIETNKKMVAQOELDYKVR 180
 DB 121 ENAERSACITGGVTNHEGHNLEIPKTIYVNSIDGISOISFDIETNKKMVAQOELDYKVR 180
 OY 181 KYLDNKKOLYTNNGPSKYEYIKFIIPKKNKESFNFDFPEPEFQSKYLMYKONETLDSN 240
 DB 181 KYLDNKKOLYTNNGPSKYEYIKFIIPKKNKESFNFDFPEPEFQSKYLMYKONETLDSN 240
 OY 241 TSQIEVYLTTR 251
 DB 241 TSQIEVYLTTR 251
 RESULT 4
 AAW59780 standard; Protein; 251 AA.
 XX AAW59780;
 AC AAW59780;
 XX 12-OCT-1998 (first entry)
 XX

DE Amino acid sequence of Streptococcus pyogenes exotoxin A.
 XX SPE-A toxin; nonlethal; mutant; Streptococcus pyogenes exotoxin A;
 KW wild type; nontoxic; antibody; vaccine; immunity; ovarian cancer;
 KW streptococcal toxic shock syndrome; STSS; T cell lymphoma;
 KW uterine cancer.
 OS Streptococcus pyogenes.
 XX
 XX MO9824911-A2.
 PN
 XX 11-JUN-1998.
 PD
 XX 05-DEC-1997; 97WO-US22228.
 PF
 XX 06-DEC-1996; 96US-0032930.
 PR
 PA (MINU) UNIV MINNESOTA.
 PI Ohlendorf D, Roggiani M, Schlievert PM, Stoehr J;
 DR WPI: 1998-333330/29.
 DR N-PSDB; AAW41593.
 XX
 XX New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention
 PT or treatment of streptococcal infection or toxic shock syndrome
 PS Disclosure; Fig 3; 95pp; English.
 XX
 XX This is the amino acid sequence of the Streptococcus pyogenes exotoxin A
 CC (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin has at least
 CC 1 aa change and is nonlethal compared with a protein to wild type SPE-A
 CC toxin. The mutant SPE-A toxins are nontoxic and can produce antibodies
 CC that neutralise wild type SPE-A toxin activity. The toxins can be used
 CC in vaccines and therapeutics to generate a protective immune response
 CC against streptococcal infection. They can be used to protect against the
 CC development of streptococcal toxic shock syndrome (STSS). In addition,
 CC the toxins can be used for treating animals with symptoms of
 CC streptococcal infection or STSS and in methods for stimulating T cell
 CC proliferation and in the treatment of cancer. In particular they can be
 CC used for treating T cell lymphomas, and ovarian and uterine cancer.
 XX
 SQ Sequence 251 AA:
 Query Match 98.9%; Score 1308; DB 19; Length 251;
 Best Local Similarity 99.2%; Pred. No. 8.3e-110;
 Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 MENNKKVYKRMVFVLTFLGLTISOEYFAQDDPSQLHRSSLYKNLONIFYLYEGDPV 60
 DB 1 MENNKKVYKRMVFVLTFLGLTISOEYFAQDDPSQLHRSSLYKNLONIFYLYEGDPV 60
 OY 61 THENKSVYDQLRSHDLIYVNSGPNYDKLTTELKNOEMATLFDKKNVDIYGEYHLCYLC 120
 DB 61 THENKSVYDQLRSHDLIYVNSGPNYDKLTTELKNOEMATLFDKKNVDIYGEYHLCYLC 120
 OY 121 ENAERSACITGGVTNHEGHNLEIPKTIYVNSIDGISOISFDIETNKKMVAQOELDYKVR 180
 DB 121 ENAERSACITGGVTNHEGHNLEIPKTIYVNSIDGISOISFDIETNKKMVAQOELDYKVR 180
 OY 181 KYLDNKKOLYTNNGPSKYEYIKFIIPKKNKESFNFDFPEPEFQSKYLMYKONETLDSN 240
 DB 181 KYLDNKKOLYTNNGPSKYEYIKFIIPKKNKESFNFDFPEPEFQSKYLMYKONETLDSN 240
 OY 241 TSQIEVYLTTR 251
 DB 241 TSQIEVYLTTR 251
 RESULT 5
 AAW12154 standard; Protein; 251 AA.
 XX AAW12154;
 AC AAW12154;
 XX

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AC AAM12154;
XX
XX 04-NOV-1997 (first entry)
XX
DE Streptococcus pyogenes Streptococcal toxin A mutant Ser195Ala.
XX
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
KW vaccine; protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
KW fever; hypotension; group A streptococcal infection; myositis;
KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
XX
OS Streptococcus pyogenes.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH 1..30
XX FT Peptide /label= sig_peptide
XX FT Peptide 31..251
XX FT /label= mat_peptide
XX FT Misc-difference 225
XX /note= "wild type Ser replaced by Ala"
XX
XX MO9640930-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US10252.
XX
XX 07-JUN-1995; 95US-0480261.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Ohlendorf D, Roggliant M, Schlievert PM, Stoehr J;
XX WPI; 1997-099936/09.
XX
XX Mutant SPE-A toxin with at least one amino acid change is
XX substantially non-lethal - used in vaccine composition for
XX treatment of cancer and streptococcal toxic shock syndrome etc.
XX
XX Example 4; Page -: 102pp; English.
XX
XX The present sequence is a non-lethal Streptococcus pyogenes
XX Streptococcal toxin A (SPE-A) mutant, which can be used to produce
XX vaccines to protect animals against wild type SPE-A and to treat
XX cancer and streptococcal toxic shock syndrome (STSS). The mutant
XX SPE-A causes neutralising antibodies (Ab) to be produced, which
XX group A streptococcal infection, myositis, e.g. fever, hypotension,
XX damage. The neutralising Ab is preferably administered in
XX conjunction with antibiotic therapy. The mutant SPE-A is
XX especially useful for treating T cell lymphomas, and ovarian and
XX uterine cancer. It is thought that mutant SPE-A can be selectively
XX toxic to T cell lymphoma cells.
XX N.B. Sequence not given in the specification, but constructed
XX using the wild type SPE-A sequence given on pages 77-79.
XX
XX Sequence 251 AA;
XX
Query Match 98.7%; Score 1305; DB 18; Length 251;
Best Local Similarity 98.8%; Pred. No. 1,5e-109;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DB 121 ENAERSACIYGVTHNEGNHLEIPKRIYVKSIDSIGSLSDIETNKKMVAQELDKVR 180
QY 181 KYLDNKKOLYTNGBPKETGYIKFIPKKESEFDFEPEPEFTQSKYLMYKNDNETLDSN 240
DB 181 KYLDNKKOLYTNGBPKETGYIKFIPKKESEFDFEPEPEFTQAKYLMYKNDNETLDSN 240
QY 241 TSQIEVYLTTR 251
DB 241 TSQIEVYLTTR 251

RESULT 6
AAM12146
ID AAM12146 standard; Protein; 251 AA.
XX
XX AAM12146;
XX
XX 04-NOV-1997 (first entry)
XX
XX Streptococcus pyogenes Streptococcal toxin A mutant Lys157Glu.
XX
XX Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
XX vaccine; protection; treatment; cancer; neutralising antibody;
XX streptococcal toxic shock syndrome; STSS; symptom; amelioration;
XX fever; hypotension; group A streptococcal infection; myositis;
XX fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
XX
XX Streptococcus pyogenes.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH 1..30
XX FT Peptide /label= sig_peptide
XX FT Peptide 31..251
XX FT /label= mat_peptide
XX FT Misc-difference 187
XX /note= "wild type Lys replaced by Glu"
XX
XX MO9640930-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US10252.
XX
XX 07-JUN-1995; 95US-0480261.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Ohlendorf D, Roggliant M, Schlievert PM, Stoehr J;
XX WPI; 1997-099936/09.
XX
XX Mutant SPE-A toxin with at least one amino acid change is
XX substantially non-lethal - used in vaccine composition for
XX treatment of cancer and streptococcal toxic shock syndrome etc.
XX
XX Claim 5; Page -: 102pp; English.
XX
XX The present sequence is a non-lethal Streptococcus pyogenes
XX Streptococcal toxin A (SPE-A) mutant, which can be used to produce
XX vaccines to protect animals against wild type SPE-A and to treat
XX cancer and streptococcal toxic shock syndrome (STSS). The mutant
XX SPE-A causes neutralising antibodies (Ab) to be produced, which
XX group A streptococcal infection, myositis, e.g. fever, hypotension,
XX damage. The neutralising Ab is preferably administered in
XX conjunction with antibiotic therapy. The mutant SPE-A is
XX especially useful for treating T cell lymphomas, and ovarian and
XX uterine cancer. It is thought that mutant SPE-A can be selectively
XX toxic to T cell lymphoma cells.
XX N.B. Sequence not given in the specification, but constructed
XX using the wild type SPE-A sequence given on pages 77-79.
XX

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xx Sequence      251 AA;
SQ
Query Match      98.6%; Score 1304; DB 18; Length 251;
Best Local Similarity 98.8%; Pred. No. 1.9e-109;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNNKRVLKKNVFFVLTFLGLTISQEVFAQDDPPSQLHRSLSLVKNLQNTIFYLEGDPV 60
DB 1 MNNKRVLKKNVFFVLTFLGLTISQEVFAQDDPPSQLHRSLSLVKNLQNTIFYLEGDPV 60
QY 61 THENKSVQDLRSHDLIYNVSGPNYDKLTTELKNQEMATLFRKKNVDIYGVEYHLCYLC 120
DB 61 THENKSVQDLRSHDLIYNVSGPNYDKLTTELKNQEMATLFRKKNVDIYGVEYHLCYLC 120
QY 121 ENAERSACIYGVTNHGSHLEIPKKIYVKVSIIDISQISLSPDIETNKKMVTQAQELDYVR 180
DB 121 ENAERSACIYGVTNHGSHLEIPKKIYVKVSIIDISQISLSPDIETNKKMVTQAQELDYVR 180
QY 181 KYLDNKKOLYTNGPSKYEYIKFIPKKNESFWDFFPEPFTQSKYLMYKDNFTLDSN 240
DB 181 KYLDNKKOLYTNGPSKYEYIKFIPKKNESFWDFFPEPFTQSKYLMYKDNFTLDSN 240
QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 7
AAW12150
ID AAW12150 standard; Protein; 251 AA.
AC AAW12150;
XX
DT 04-NOV-1997 (first entry)
XX
DE Streptococcus pyogenes Streptococcal toxin A mutant Lys1Asn.
XX
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
KW vaccine; protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
KW fever; hypotension; group A streptococcal infection; myositis;
KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
XX
OS Streptococcus pyogenes.
OS Synthetic.
XX
FH Key Location/Qualifiers
FH Peptide 1..30
FT /label= sig_peptide
FT Peptide 31..251
FT /label= mat_peptide
FT Misc-difference 46
FT /note= "wild type Lys replaced by Asn"
XX
XX W09640930-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US10252.
XX
XX 07-JUN-1995; 95US-0480261.
XX
XX (MIND ) UNIV MINNESOTA.
XX
XX Ohlendorf D, Roggiani M, Schlievert PM, Stoehr J;
XX
XX WPI; 1997-099936/09.
XX
XX Mutant SPE-A toxin with at least one amino acid change is
XX substantially non-lethal - used in vaccine composition for
XX treatment of cancer and streptococcal toxic shock syndrome etc.
XX

```

```

PS Example 4; Page -: 102pp; English.
XX
XX The present sequence is a non-lethal Streptococcus pyogenes
CC Streptococcal toxin A (SPE-A) mutant, which can be used to produce
CC vaccines to protect animals against wild type SPE-A and to treat
CC cancer and streptococcal toxic shock syndrome (STSS). The mutant
CC SPE-A causes neutralising antibodies (Ab) to be produced, which
CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
CC group A streptococcal infection, myositis, fasciitis and liver
CC damage. The neutralising Ab is preferably administered in
CC conjunction with antibiotic therapy. The mutant SPE-A is
CC especially useful for treating T cell lymphomas, and ovarian and
CC uterine cancer. It is thought that mutant SPE-A can be selectively
CC toxic to T cell lymphoma cells.
CC N.B. Sequence not given in the specification, but constructed
CC using the wild type SPE-A sequence given on pages 77-79.
XX
SQ Sequence .251 AA;

Query Match      98.6%; Score 1303; DB 18; Length 251;
Best Local Similarity 98.8%; Pred. No. 2.3e-109;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNNKRVLKKNVFFVLTFLGLTISQEVFAQDDPPSQLHRSLSLVKNLQNTIFYLEGDPV 60
DB 1 MNNKRVLKKNVFFVLTFLGLTISQEVFAQDDPPSQLHRSLSLVKNLQNTIFYLEGDPV 60
QY 61 THENKSVQDLRSHDLIYNVSGPNYDKLTTELKNQEMATLFRKKNVDIYGVEYHLCYLC 120
DB 61 THENKSVQDLRSHDLIYNVSGPNYDKLTTELKNQEMATLFRKKNVDIYGVEYHLCYLC 120
QY 121 ENAERSACIYGVTNHGSHLEIPKKIYVKVSIIDISQISLSPDIETNKKMVTQAQELDYVR 180
DB 121 ENAERSACIYGVTNHGSHLEIPKKIYVKVSIIDISQISLSPDIETNKKMVTQAQELDYVR 180
QY 181 KYLDNKKOLYTNGPSKYEYIKFIPKKNESFWDFFPEPFTQSKYLMYKDNFTLDSN 240
DB 181 KYLDNKKOLYTNGPSKYEYIKFIPKKNESFWDFFPEPFTQSKYLMYKDNFTLDSN 240
QY 241 TSQIEVYLTTK 251
DB 241 TSQIEVYLTTK 251

RESULT 8
AAW12147
ID AAW12147 standard; Protein; 251 AA.
AC AAW12147;
XX
DT 04-NOV-1997 (first entry)
XX
DE Streptococcus pyogenes Streptococcal toxin A mutant Asn20Asp.
XX
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
KW vaccine; protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
KW fever; hypotension; group A streptococcal infection; myositis;
KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
XX
OS Streptococcus pyogenes.
OS Synthetic.
XX
FH Key Location/Qualifiers
FH Peptide 1..30
FT /label= sig_peptide
FT Peptide 31..251
FT /label= mat_peptide
FT Misc-difference 50
FT /note= "wild type Asn replaced by Asp"
XX
XX W09640930-A1.
XX

```

PD 19-DEC-1996.
 XX 07-JUN-1996; 96WO-US10252.
 XX 07-JUN-1995; 95US-0480261.
 XX (MINU) UNIV MINNESOTA.
 XX Ohlendorf D, Roggliani M, Schlievert PM, Stoehr J;
 DR WPI: 1997-099936/09.
 XX
 XX Mutant SPE-A toxin with at least one amino acid change is
 PT substantially non-lethal - used in vaccine composition for
 PT treatment of cancer and streptococcal toxic shock syndrome etc.
 PS
 PS Claim 5; Page -: 102pp; English.
 XX
 XX The present sequence is a non-lethal Streptococcus pyogenes
 CC Streptococcal toxin A (SPE-A) mutant, which can be used to produce
 CC vaccines to protect animals against wild type SPE-A and to treat
 CC cancer and streptococcal toxic shock syndrome (STSS). The mutant
 CC SPE-A causes neutralising antibodies (Ab) to be produced, which
 CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
 CC group A streptococcal infection, myositis, fasciitis and liver
 CC damage. The neutralising Ab is preferably administered in
 CC conjunction with antibiotic therapy. The mutant SPE-A is
 CC especially useful for treating T cell lymphomas, and ovarian and
 CC uterine cancer. It is thought that mutant SPE-A can be selectively
 CC toxic to T cell lymphoma cells.
 CC N.B. Sequence not given in the specification, but constructed
 CC using the wild type SPE-A sequence given on pages 77-79.
 XX
 SO Sequence 251 AA;

Query Match 98.6%; Score 1303; DB 18; Length 251;
 Best Local Similarity 98.8%; Pred. No. 2.3e-109;
 Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNNKKVLLKKMVFVLTFLGLTISQEVFAQODPDSQLRSSLVKNLNIYFLYEGDPV 60
 DB 1 MNNKKVLLKKMVFVLTFLGLTISQEVFAQODPDSQLRSSLVKNLNIYFLYEGDPV 60
 QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKNOEMATLFFKKNVDIYGEVYHLCYLC 120
 DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKNOEMATLFFKKNVDIYGEVYHLCYLC 120
 QY 121 ENAERSACIYGVYTNHGNHLEIPKRIYVVSIDGQSLSFDLETNKKMTAQLDYKVR 180
 DB 121 ENAERSACIYGVYTNHGNHLEIPKRIYVVSIDGQSLSFDLETNKKMTAQLDYKVR 180
 QY 121 ENAERSACIYGVYTNHGNHLEIPKRIYVVSIDGQSLSFDLETNKKMTAQLDYKVR 180
 DB 121 ENAERSACIYGVYTNHGNHLEIPKRIYVVSIDGQSLSFDLETNKKMTAQLDYKVR 180
 QY 181 KYLTDNKQLYTNNGPSKYEYIKFIPKNKSEFDFPEPEFOSKYLMIYKONETLDSN 240
 DB 181 KYLTDNKQLYTNNGPSKYEYIKFIPKNKSEFDFPEPEFOSKYLMIYKONETLDSN 240
 QY 241 TSOIEVYLYTRK 251
 DB 241 TSOIEVYLYTRK 251

RESULT 9
 AAM12148
 ID AAM12148 standard; Protein; 251 AA.

XX AAM12148;
 XX

XX 04-NOV-1997 (first entry)
 XX

DE Streptococcus pyogenes Streptococcal toxin A mutant N20D/K157E.
 XX

KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
 KM vaccine; protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;

KW fever; hypotension; group A streptococcal infection; myositis;
 KM fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
 XX
 XX Streptococcus pyogenes.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..30
 FT /label- sig_peptide
 FT Peptide 31..251
 FT /label- mat_peptide
 FT Misc-difference 50
 FT /note- "wild type Asn replaced by Asp"
 FT Misc-difference 187
 FT /note- "wild type Lys replaced by Glu"

MO9640930-A1.

19-DEC-1996.

07-JUN-1996; 96WO-US10252.

07-JUN-1995; 95US-0480261.

(MINU) UNIV MINNESOTA.

Ohlendorf D, Roggliani M, Schlievert PM, Stoehr J;

WPI: 1997-099936/09.

PT Mutant SPE-A toxin with at least one amino acid change is
 PT substantially non-lethal - used in vaccine composition for
 PT treatment of cancer and streptococcal toxic shock syndrome etc.

PS Claim 5; Page -: 102pp; English.

XX
 XX The present sequence is a non-lethal Streptococcus pyogenes
 CC Streptococcal toxin A (SPE-A) mutant, which can be used to produce
 CC vaccines to protect animals against wild type SPE-A and to treat
 CC cancer and streptococcal toxic shock syndrome (STSS). The mutant
 CC SPE-A causes neutralising antibodies (Ab) to be produced, which
 CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
 CC group A streptococcal infection, myositis, fasciitis and liver
 CC damage. The neutralising Ab is preferably administered in
 CC conjunction with antibiotic therapy. The mutant SPE-A is
 CC especially useful for treating T cell lymphomas, and ovarian and
 CC uterine cancer. It is thought that mutant SPE-A can be selectively
 CC toxic to T cell lymphoma cells.
 CC N.B. Sequence not given in the specification, but constructed
 CC using the wild type SPE-A sequence given on pages 77-79.

SO Sequence 251 AA;

Query Match 98.3%; Score 1299; DB 18; Length 251;
 Best Local Similarity 98.4%; Pred. No. 5.4e-109;
 Matches 247; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNNKKVLLKKMVFVLTFLGLTISQEVFAQODPDSQLRSSLVKNLNIYFLYEGDPV 60
 DB 1 MNNKKVLLKKMVFVLTFLGLTISQEVFAQODPDSQLRSSLVKNLNIYFLYEGDPV 60
 QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKNOEMATLFFKKNVDIYGEVYHLCYLC 120
 DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKNOEMATLFFKKNVDIYGEVYHLCYLC 120
 QY 121 ENAERSACIYGVYTNHGNHLEIPKRIYVVSIDGQSLSFDLETNKKMTAQLDYKVR 180
 DB 121 ENAERSACIYGVYTNHGNHLEIPKRIYVVSIDGQSLSFDLETNKKMTAQLDYKVR 180
 QY 121 ENAERSACIYGVYTNHGNHLEIPKRIYVVSIDGQSLSFDLETNKKMTAQLDYKVR 180
 DB 121 ENAERSACIYGVYTNHGNHLEIPKRIYVVSIDGQSLSFDLETNKKMTAQLDYKVR 180
 QY 181 KYLTDNKQLYTNNGPSKYEYIKFIPKNKSEFDFPEPEFOSKYLMIYKONETLDSN 240
 DB 181 KYLTDNKQLYTNNGPSKYEYIKFIPKNKSEFDFPEPEFOSKYLMIYKONETLDSN 240

OY 241 TSOIEVYLTWK 251
 DB 241 TSOIEVYLTWK 251

RESULT 10

AAW12151
 ID AAW12151 standard; Protein: 251 AA.

XX AAW12151;

DT 04-NOV-1997 (first entry)

DE Streptococcus pyogenes Streptococcal toxin A mutant Cys87Ser.

KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
 KW vaccine; protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
 KW fever; hypotension; group A streptococcal infection; myositis;
 KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.

OS Streptococcus pyogenes.
 OS Synthetic.

FT Key Location/Qualifiers

FT Peptide 1..30

FT /label- sig_peptide

FT Peptide 31..251

FT /label- mat_peptide

FT Misc-difference 117 /note- "wild type Cys replaced by Ser"

XX MO9640930-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US10252.

XX 07-JUN-1995; 95US-0480261.

XX (MINU) UNIV MINNESOTA.

XX Ohlendorf D, Roggliani M, Schlievert PM, Stoehr J;

XX WPI; 1997-099936/09.

PT Mutant SPE-A toxin with at least one amino acid change is
 PT substantially non-lethal - used in vaccine composition for
 PT treatment of cancer and streptococcal toxic shock syndrome etc.

XX Example 4; Page -: 102pp; English.

CC The present sequence is a non-lethal Streptococcus pyogenes
 CC Streptococcal toxin A (SPE-A) mutant, which can be used to produce
 CC vaccines to protect animals against wild type SPE-A and to treat
 CC cancer and streptococcal toxic shock syndrome (STSS). The mutant
 CC SPE-A causes neutralising antibodies (Ab) to be produced, which
 CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
 CC group A streptococcal infection, myositis, fasciitis and liver
 CC damage. The neutralising Ab is preferably administered in
 CC conjunction with antibiotic therapy. The mutant SPE-A is
 CC especially useful for treating T cell lymphomas, and ovarian and
 CC uterine cancer. It is thought that mutant SPE-A can be selectively
 CC toxic to T cell lymphoma cells.
 CC N.B. Sequence not given in the specification, but constructed
 CC using the wild type SPE-A sequence given on pages 77-79.

XX Sequence 251 AA;

Query Match 98.2%; Score 1298; DB 18; Length 251;
 Best Local Similarity 98.8%; Pred. No. 6.6e-109;
 Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 MNNKKVLLKRVFVLTFLGTTISQEVFAQODPPPSQLHRSLSLVKNLQNTLYLEGDPV 60
 DB 1 MNNKKVLLKRVFVLTFLGTTISQEVFAQODPPPSQLHRSLSLVKNLQNTLYLEGDPV 60
 OY 61 THENKVSVDQLRSHDLIYNVSGPNYDKLTTELKQEMATLFRKNVDIYGEVYHLCYLC 120
 DB 61 THENKVSVDQLRSHDLIYNVSGPNYDKLTTELKQEMATLFRKNVDIYGEVYHLSTLC 120
 OY 121 ENAERSACIYGVNTHNHCNHLFIRKKIYKVSIDIGISLSDIETNKKMTVAQELDKYVR 180
 DB 121 ENAERSACIYGVNTHNHCNHLFIRKKIYKVSIDIGISLSDIETNKKMTVAQELDYKVR 180
 OY 181 KYLTDNKLTYNGSPSKYETGYIKFIPKKNESFMDPFPPEPTOSKYLMTIKDNETLDSN 240
 DB 181 KYLTDNKLTYNGSPSKYETGYIKFIPKKNESFMDPFPPEPTOSKYLMTIKDNETLDSN 240
 OY 241 TSOIEVYLTWK 251
 DB 241 TSOIEVYLTWK 251

RESULT 11

AAW12152
 ID AAW12152 standard; Protein: 251 AA.

XX AAW12152;

DT 04-NOV-1997 (first entry)

DE Streptococcus pyogenes Streptococcal toxin A mutant Cys98Ser.

KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
 KW vaccine; protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
 KW fever; hypotension; group A streptococcal infection; myositis;
 KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.

OS Streptococcus pyogenes.
 OS Synthetic.

FT Key Location/Qualifiers

FT Peptide 1..30

FT /label- sig_peptide

FT Peptide 31..251

FT /label- mat_peptide

FT Misc-difference 128 /note- "wild type Cys replaced by Ser"

XX MO9640930-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US10252.

XX 07-JUN-1995; 95US-0480261.

XX (MINU) UNIV MINNESOTA.

XX Ohlendorf D, Roggliani M, Schlievert PM, Stoehr J;

XX WPI; 1997-099936/09.

PT Mutant SPE-A toxin with at least one amino acid change is
 PT substantially non-lethal - used in vaccine composition for
 PT treatment of cancer and streptococcal toxic shock syndrome etc.

XX Example 4; Page -: 102pp; English.

CC The present sequence is a non-lethal Streptococcus pyogenes
 CC Streptococcal toxin A (SPE-A) mutant, which can be used to produce
 CC vaccines to protect animals against wild type SPE-A and to treat
 CC cancer and streptococcal toxic shock syndrome (STSS). The mutant
 CC SPE-A causes neutralising antibodies (Ab) to be produced, which

CC may be used to ameliorate STSS symptoms, e.g., fever, hypotension,
 CC group A streptococcal infection, myositis, fasciitis and liver
 CC damage. The neutralising Ab is preferably administered in
 CC conjunction with antibiotic therapy. The mutant SPE-A is
 CC especially useful for treating T cell lymphomas, and ovarian and
 CC uterine cancer. It is thought that mutant SPE-A can be selectively
 CC toxic to T cell lymphoma cells.
 CC N.B. Sequence not given in the specification, but constructed
 CC using the wild type SPE-A sequence given on pages 77-79.

XX Sequence 251 AA;

Query Match 98.2%; Score 1298; DB 18; Length 251;
 Best Local Similarity 98.8%; Pred. No. 6.6e-109;
 Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 MENKKVLLKKMVFVLTFLGTLTISQEVFAQODDPQSOLHRSSLVKNLQNTYFLYEGDPV 60
 DB 1 MENKKVLLKKMVFVLTFLGTLTISQEVFAQODDPQSOLHRSSLVKNLQNTYFLYEGDPV 60
 OY 61 THENVKSVDOLRSHDLIYVNSGPNYDKLTETLKNQEMATLFRKDNVDIYGEVYHLCYLC 120
 DB 61 THENVKSVDOLRSHDLIYVNSGPNYDKLTETLKNQEMATLFRKDNVDIYGEVYHLCYLC 120
 OY 121 ENAERSACIYGVYTNHSGNHLIPIPKIIVKVSIDGISLSFDIETNKKMVTAGQLDYKVR 180
 DB 121 ENAERSACIYGVYTNHSGNHLIPIPKIIVKVSIDGISLSFDIETNKKMVTAGQLDYKVR 180
 OY 121 ENAERSACIYGVYTNHSGNHLIPIPKIIVKVSIDGISLSFDIETNKKMVTAGQLDYKVR 180
 DB 121 ENAERSACIYGVYTNHSGNHLIPIPKIIVKVSIDGISLSFDIETNKKMVTAGQLDYKVR 180
 OY 181 KYLDNKLQVLTNGSKYETGYIKRIPKKNESFMPDFPEPTOSKILMIYKDNETIDSN 240
 DB 181 KYLDNKLQVLTNGSKYETGYIKRIPKKNESFMPDFPEPTOSKILMIYKDNETIDSN 240
 OY 241 TSQIEVYLTTR 251
 DB 241 TSQIEVYLTTR 251

RESULT 12

AAW12153
 ID AAW12153 standard; Protein; 251 AA.

XX AAW12153;

DT 04-NOV-1997 (first entry)

DE Streptococcus pyogenes Streptococcal toxin A mutant Cys90Ser.

KW Streptococcal: toxin A; SPE-A; non-lethal; mutant; production;
 KW vaccine; protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
 KW fever; hypotension; group A streptococcal infection; myositis;
 KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.

XX Streptococcus pyogenes.
 OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..30

FT Peptide /label- sig-peptide

FT Peptide /label- mat-peptide

FT Misc-difference 120 /note= "wild type Cys replaced by Ser"

XX W09640930-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US10252.

XX 07-JUN-1995; 95US-0480261.

XX (MINU) UNIV MINNESOTA.

XX Ohlendorf D, Roggiani M, Schlievert PM, Stoehr J;
 XX WPI: 1997-099936/09.

PT Mutant SPE-A toxin with at least one amino acid change is
 PT substantially non-lethal - used in vaccine composition for
 PT treatment of cancer and streptococcal toxic shock syndrome etc.
 XX Example 4; Page -: 102pp; English.

XX The present sequence is a non-lethal Streptococcus pyogenes
 CC Streptococcal toxin A (SPE-A) mutant, which can be used to produce
 CC vaccines to protect animals against wild type SPE-A and to treat
 CC cancer and streptococcal toxic shock syndrome (STSS). The mutant
 CC SPE-A causes neutralising antibodies (Ab) to be produced, which
 CC may be used to ameliorate STSS symptoms, e.g., fever, hypotension,
 CC group A streptococcal infection, myositis, fasciitis and liver
 CC damage. The neutralising Ab is preferably administered in
 CC conjunction with antibiotic therapy. The mutant SPE-A is
 CC especially useful for treating T cell lymphomas, and ovarian and
 CC uterine cancer. It is thought that mutant SPE-A can be selectively
 CC toxic to T cell lymphoma cells.
 CC N.B. Sequence not given in the specification, but constructed
 CC using the wild type SPE-A sequence given on pages 77-79.

XX Sequence 251 AA;

Query Match 98.2%; Score 1298; DB 18; Length 251;
 Best Local Similarity 98.8%; Pred. No. 6.6e-109;
 Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 MENKKVLLKKMVFVLTFLGTLTISQEVFAQODDPQSOLHRSSLVKNLQNTYFLYEGDPV 60
 DB 1 MENKKVLLKKMVFVLTFLGTLTISQEVFAQODDPQSOLHRSSLVKNLQNTYFLYEGDPV 60
 OY 61 THENVKSVDOLRSHDLIYVNSGPNYDKLTETLKNQEMATLFRKDNVDIYGEVYHLCYLC 120
 DB 61 THENVKSVDOLRSHDLIYVNSGPNYDKLTETLKNQEMATLFRKDNVDIYGEVYHLCYLC 120
 OY 121 ENAERSACIYGVYTNHSGNHLIPIPKIIVKVSIDGISLSFDIETNKKMVTAGQLDYKVR 180
 DB 121 ENAERSACIYGVYTNHSGNHLIPIPKIIVKVSIDGISLSFDIETNKKMVTAGQLDYKVR 180
 OY 181 KYLDNKLQVLTNGSKYETGYIKRIPKKNESFMPDFPEPTOSKILMIYKDNETIDSN 240
 DB 181 KYLDNKLQVLTNGSKYETGYIKRIPKKNESFMPDFPEPTOSKILMIYKDNETIDSN 240
 OY 241 TSQIEVYLTTR 251
 DB 241 TSQIEVYLTTR 251

RESULT 13

AAW12149
 ID AAW12149 standard; Protein; 251 AA.

XX AAW12149;

DT 04-NOV-1997 (first entry)

DE Streptococcus pyogenes Streptococcal toxin A mutant N20D/C98S.

KW Streptococcal: toxin A; SPE-A; non-lethal; mutant; production;
 KW vaccine; protection; treatment; cancer; neutralising antibody;
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
 KW fever; hypotension; group A streptococcal infection; myositis;
 KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.

XX Streptococcus pyogenes.
 OS Synthetic.

XX Key Location/Qualifiers

```

FT Peptide 1..30
FT /label- sig_peptide
FT Peptide 31..251
FT /label- mat_peptide
FT Misc-difference 50
FT /note- "wild type Asn replaced by Asp"
FT Misc-difference 128
FT /note- "wild type Cys replaced by Ser"
XX
XX W09640930-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96MO-US10252.
XX
XX 07-JUN-1995; 95US-0480261.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Ohlendorf D, Roggiani M, Schlievert PM, Stoehr J;
XX WPI; 1997-099936/09.
XX
XX Mutant SPE-A toxin with at least one amino acid change is
XX substantially non-lethal - used in vaccine composition for
XX treatment of cancer and streptococcal toxic shock syndrome etc.
XX
XX Claim 5; Page -: 102pp; English.
XX
XX The present sequence is a non-lethal Streptococcus pyogenes
XX Streptococcal toxin A (SPE-A) mutant, which can be used to produce
XX vaccines to protect animals against wild type SPE-A and to treat
XX cancer and streptococcal toxic shock syndrome (STSS). The mutant
XX SPE-A causes neutralising antibodies (Ab) to be produced, which
XX may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
XX group A streptococcal infection, myositis, fasciitis and liver
XX damage. The neutralising Ab is preferably administered in
XX conjunction with antibiotic therapy. The mutant SPE-A is
XX especially useful for treating T cell lymphomas, and ovarian and
XX uterine cancer. It is thought that mutant SPE-A can be selectively
XX toxic to T cell lymphoma cells.
XX N.B. Sequence not given in the specification, but constructed
XX using the wild type SPE-A sequence given on pages 77-79.
XX
XX Sequence 251 AA;
XX
XX Query Match 97.8%; Score 1293; DB 18; Length 251;
XX Best Local Similarity 98.4%; Pred. No. 1.9e-108;
XX Matches 247; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 MENNKVYLKKMVFVLTFLGLTISOEVFAQODDPQSOLHRSSLVKMLQNTYFLYEGDPV 60
XX 1 MENNKVYLKKMVFVLTFLGLTISOEVFAQODDPQSOLHRSSLVKMLQNTYFLYEGDPV 60
XX
XX 61 THENVKSVDOLRSHDLIYNVSGPNYDKLTKELKQENATLFEKDNVDIYGEVYHLCYL 120
XX 61 THENVKSVDOLRSHDLIYNVSGPNYDKLTKELKQENATLFEKDNVDIYGEVYHLCYL 120
XX
XX 121 ENAERSACIYGGVYTNHSGNHLIPEPKIIVKVSIDIGIOSLSFSDIETNKKMVTYAOELDYKVR 180
XX 121 ENAERSACIYGGVYTNHSGNHLIPEPKIIVKVSIDIGIOSLSFSDIETNKKMVTYAOELDYKVR 180
XX
XX 121 ENAERSACIYGGVYTNHSGNHLIPEPKIIVKVSIDIGIOSLSFSDIETNKKMVTYAOELDYKVR 180
XX 121 ENAERSACIYGGVYTNHSGNHLIPEPKIIVKVSIDIGIOSLSFSDIETNKKMVTYAOELDYKVR 180
XX
XX 181 KYLTDNKOYLTNGPSKRTGYIKFIPKNKSFDFPEPEPTOSKILMITYKONETLDSN 240
XX 181 KYLTDNKOYLTNGPSKRTGYIKFIPKNKSFDFPEPEPTOSKILMITYKONETLDSN 240
XX
XX 241 TSQIEVYLTTR 251
XX 241 TSQIEVYLTTR 251
XX
XX Db 241 TSQIEVYLTTR 251
XX
XX RESULT 14
XX AAM12145

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ID AAM12145 standard; Protein; 250 AA.
XX
XX AAM12145;
XX
XX 04-NOV-1997 (first entry)
XX
XX Streptococcus pyogenes Streptococcal toxin A mutant delta98.
XX
XX Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
XX vaccine; protection; treatment; cancer; neutralising antibody;
XX streptococcal toxic shock syndrome; STSS; symptom; amelioration;
XX fever; hypotension; group A streptococcal infection; myositis;
XX fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
XX
XX Streptococcus pyogenes.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..30
XX /label- sig_peptide
XX Peptide 31..250
XX /label- mat_peptide
XX
XX W09640930-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96MO-US10252.
XX
XX 07-JUN-1995; 95US-0480261.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Ohlendorf D, Roggiani M, Schlievert PM, Stoehr J;
XX WPI; 1997-099936/09.
XX
XX Mutant SPE-A toxin with at least one amino acid change is
XX substantially non-lethal - used in vaccine composition for
XX treatment of cancer and streptococcal toxic shock syndrome etc.
XX
XX Claim 5; Page -: 102pp; English.
XX
XX The present sequence is a non-lethal Streptococcus pyogenes
XX Streptococcal toxin A (SPE-A) mutant, which can be used to produce
XX vaccines to protect animals against wild type SPE-A and to treat
XX cancer and streptococcal toxic shock syndrome (STSS). The mutant
XX SPE-A causes neutralising antibodies (Ab) to be produced, which
XX may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
XX group A streptococcal infection, myositis, fasciitis and liver
XX damage. The neutralising Ab is preferably administered in
XX conjunction with antibiotic therapy. The mutant SPE-A is
XX especially useful for treating T cell lymphomas, and ovarian and
XX uterine cancer. It is thought that mutant SPE-A can be selectively
XX toxic to T cell lymphoma cells.
XX N.B. Sequence not given in the specification, but constructed
XX using the wild type SPE-A sequence given on pages 77-79.
XX
XX Sequence 250 AA;
XX
XX Query Match 97.5%; Score 1288.5; DB 18; Length 250;
XX Best Local Similarity 98.8%; Pred. No. 4.7e-108;
XX Matches 248; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
XX
XX 1 MENNKVYLKKMVFVLTFLGLTISOEVFAQODDPQSOLHRSSLVKMLQNTYFLYEGDPV 60
XX 1 MENNKVYLKKMVFVLTFLGLTISOEVFAQODDPQSOLHRSSLVKMLQNTYFLYEGDPV 60
XX
XX 61 THENVKSVDOLRSHDLIYNVSGPNYDKLTKELKQENATLFEKDNVDIYGEVYHLCYL 120
XX 61 THENVKSVDOLRSHDLIYNVSGPNYDKLTKELKQENATLFEKDNVDIYGEVYHLCYL 120
XX
XX 121 ENAERSACIYGGVYTNHSGNHLIPEPKIIVKVSIDIGIOSLSFSDIETNKKMVTYAOELDYKVR 180
XX 121 ENAERSACIYGGVYTNHSGNHLIPEPKIIVKVSIDIGIOSLSFSDIETNKKMVTYAOELDYKVR 180
XX
XX Db 61 THENVKSVDOLRSHDLIYNVSGPNYDKLTKELKQENATLFEKDNVDIYGEVYHLCYL 120
XX
XX RESULT 14
XX AAM12145

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Db      121 ENAERSA-IYGVTHHEGHNHLEIPKKIYVKVSIIDGISLSPDIEFTNKKMTVAQELDYKVR 179
Oy      181 KYLDNKKQLYTNGSPSKYETGYIKFIPKKNKESFDFPEPEPTOSKYLMIYKDNETLDSN 240
Db      180 KYLDNKKQLYTNGSPSKYETGYIKFIPKKNKESFDFPEPEPTOSKYLMIYKDNETLDSN 239
Oy      241 TSQIEVYLLTK 251
Db      240 TSQIEVYLLTK 250

RESULT 15
AAW59798
ID      AAW59798 standard; Protein; 251 AA.
XX      AAW59798;
AC      AAW59798;
XX      12-OCT-1998 (first entry)
DE      Amino acid sequence of mutant Streptococcus pyogenes exotoxin A.
XX      SPE-A toxin; nonlethal; mutant: Streptococcus pyogenes exotoxin A;
XX      wild type: nontoxic; antibody; vaccine; immunity; ovarian cancer;
XX      streptococcal toxic shock syndrome; STSS; T cell lymphoma;
XX      uterine cancer.
XX      Streptococcus pyogenes.
XX      Key      Location/Qualifiers
FH      Misc-difference 20
FT      /note= "optionally Asp, Glu, Lys, or Arg"
FT      Misc-difference 45
FT      /note= "optionally Asp, Glu, Ser, Thr, or Ala"
FT      Misc-difference 98
FT      /note= "optionally Ser, Ala, Gly, or Thr"
FT      Misc-difference 157
FT      /note= "optionally Glu or Asp"
XX      W09824911-A2.
XX      11-JUN-1998.
XX      05-DEC-1997; 97MO-US22228.
XX      06-DEC-1996; 96US-0032930.
XX      (MINU ) UNIV MINNESOTA.
XX      Ohlendorf D, Roggiani M, Schlievert PW, Stoehr J;
XX      WPI; 1998-333330/29.
XX      New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention
XX      or treatment of streptococcal infection or toxic shock syndrome
XX      Claim 4; Page -: 95pp; English.
XX      This is the amino acid sequence of the mutant Streptococcus pyogenes
XX      exotoxin A (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin
XX      has at least 1 aa change and is nonlethal compared with a protein to
XX      wild type SPE-A toxin. The mutant SPE-A toxins are nonlethal and can
XX      produce antibodies that neutralise wild type SPE-A toxin activity. The
XX      toxins can be used in vaccines and therapeutics to generate a protective
XX      immune response against streptococcal infection. They can be used to
XX      protect against the development of streptococcal toxic shock syndrome
XX      (STSS). In addition, the toxins can be used for treating animals with
XX      symptoms of streptococcal infection or STSS and in methods for
XX      stimulating T cell proliferation and in the treatment of cancer. In
XX      particular they can be used for treating T cell lymphomas, and ovarian
XX      and uterine cancer.
XX      This sequence was not present in the specification but was created
XX      using information given.

```

```

XX      SQ      sequence      251 AA;
Oy      Query Match      97.4%; Score 1288; DB 19; Length 251;
Oy      Best Local Similarity 97.6%; Pred. No. 5.3e-108;
Oy      Matches 245; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Db      1 MENNKKVLLKKWFFVLVTFELGTTISOEVFAQDDPDSQLHRSLSLVKNLONTYFLYEGDPV 60
Oy      1 MENNKKVLLKKWFFVLVTFELGTTISOEVFAQDDPDSQLHRSLSLVKNLONTYFLYEGDPV 60
Db      61 THENVKSVDQLSHDLIYNVSGPNYDKLTTELKQEMATLPRKKNVDIYGVYHLCTYC 120
Oy      61 THENVKSVDQLSHDLIYNVSGPNYDKLTTELKQEMATLPRKKNVDIYGVYHLCTYC 120
Db      121 ENAERSACIYGVTHHEGHNHLEIPKKIYVKVSIIDGISLSPDIEFTNKKMTVAQELDYKVR 180
Oy      121 ENAERSACIYGVTHHEGHNHLEIPKKIYVKVSIIDGISLSPDIEFTNKKMTVAQELDYKVR 180
Db      121 ENAERSACIYGVTHHEGHNHLEIPKKIYVKVSIIDGISLSPDIEFTNKKMTVAQELDYKVR 180
Oy      181 KYLDNKKQLYTNGSPSKYETGYIKFIPKKNKESFDFPEPEPTOSKYLMIYKDNETLDSN 240
Db      181 KYLDNKKQLYTNGSPSKYETGYIKFIPKKNKESFDFPEPEPTOSKYLMIYKDNETLDSN 240
Oy      241 TSQIEVYLLTK 251
Oy      241 TSQIEVYLLTK 251
Db      241 TSQIEVYLLTK 251

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Search completed: June 23, 2003, 16:12:24
Job time : 38.6551 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 16:06:15 ; Search time 68.3449 seconds

(without alignments)
912.449 Million cell updates/sec

File: US-10-002-784A-27

Perfect score: 2500
Sequence: 1 MQDDPDSQLHRSSLVKMLQ.....ALGTGAGAGFNGYSAYVG 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

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3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
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16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
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18: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
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21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1327.5	53.1	398	17	AAW07898	Streptococcus pyog
2	1327.5	53.1	398	17	AAW07898	Streptococcus pyog
3	1327.5	53.1	398	21	AAV81812	S. pyogenes speb g
4	1323.5	52.9	398	23	ABP29579	Streptococcus cystei
5	1195.5	47.8	398	21	AAW36098	Streptococcus poly
6	1136	45.4	251	21	AAV70109	Streptococcus pyog
7	1136	45.4	251	23	ABP79508	Streptococcus pyro
8	1129	44.9	221	22	AAW67344	Streptococcus pyro
9	1123	44.9	221	12	AAW13209	Streptococcus pyro
10	1123	44.9	221	14	AAW45017	Staphylococcus ent

11	1123	44.9	221	23	ABW6240	Staphylococcus pyo
12	1122	44.9	251	18	AAW12097	Streptococcus pyog
13	1122	44.9	251	19	AAW59780	Amino acid sequenc
14	1119	44.8	251	18	AAW12154	Streptococcus pyog
15	1118	44.7	251	18	AAW12146	Streptococcus pyog
16	1117.5	44.7	250	18	AAW12145	Streptococcus pyog
17	1117	44.7	251	18	AAW12150	Streptococcus pyog
18	1117	44.7	251	18	AAW12147	Streptococcus pyog
19	1113	44.5	251	18	AAW12148	Streptococcus pyog
20	1112	44.5	251	18	AAW12151	Streptococcus pyog
21	1112	44.5	251	18	AAW12152	Streptococcus pyog
22	1112	44.5	251	18	AAW12153	Streptococcus pyog
23	1107	44.3	251	18	AAW12149	Streptococcus pyog
24	1107	44.3	251	19	AAW59781	Amino acid sequenc
25	1107	44.3	251	19	AAW59798	Amino acid sequenc
26	543	21.7	239	19	AAW64647	Synthetic SEB prot
27	541	21.6	239	22	AAW67341	Staphylococcus aur
28	541	21.6	255	18	AAW06737	Staphylococcus aur
29	539	21.6	266	21	AAV92319	Plant-optimized mu
30	532	21.3	266	23	ABW79503	Staphylococcus ent
31	530	21.2	239	23	ABW79505	Staphylococcus ent
32	530	21.2	240	21	AAV54465	Mutant Staphylococ
33	530	21.2	266	21	AAV54464	Amino acid sequenc
34	528	21.1	239	12	AAW13206	Staphylococcus ent
35	528	21.1	239	14	AAW45014	Staphylococcus ent
36	527	21.1	239	23	ABW76237	Staphylococcus aur
37	525	21.0	239	21	AAV70106	Mutant Staphylococ
38	523	20.9	266	23	ABW79504	Staphylococcus ent
39	514	20.6	266	21	AAV70108	Staphylococcus ent
40	514	20.6	266	23	ABW79507	Staphylococcus SEC
41	513.5	20.5	265	21	AAV70104	Staphylococcus ent
42	513	20.5	239	20	AAW06254	Staphylococcus gro
43	511	20.4	238	13	ABW76239	Staphylococcus aur
44	510	20.4	238	14	AAW45016	Staphylococcus ent
45	510	20.4	238	22	AAW67343	Staphylococcus aur

ALIGNMENTS

```

RESULT 1
AAW07898
ID AAW07898 standard; Protein; 398 AA.
AC AAW07898;
XX
XX
XX 22-JUL-1997 (first entry)
DE Streptococcus pyogenes clone speB7 pre-pro cysteine protease.
XX
XX
XX Pre-pro: cysteine; protease; inhibition; neoplastic; proliferation;
KW cell; human; treatment; carcinoma; sarcoma; melanoma; lymphoma;
KW leukemia; leukemia; blood; lung; mammary gland; prostate;
KW intestine; stomach; liver; heart; skin; pancreas; brain tissue;
KW wound covering; prevention; metastasis; identification; speB7.
XX
XX Streptococcus pyogenes.
OS
XX
XX
XX Key Location/Qualifiers
XX FT MISC-difference 216
XX FT /note="corresponding codon TAG"
XX FT 333..338
XX FT Domain /label= nucleotide_binding_domain
XX
XX WO9634941-A1.
XX
XX 07-NOV-1996.
XX
XX 30-APR-1996; 96MO-US05997.
XX
XX 01-MAY-1995; 95US-0432692.
XX
XX (BAYU ) BAYLOR COLLEGE MEDICINE.

```

PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Ananthaswamy HN, Fernandez A, Kapur V, Musser JM;
 XX
 DR WPI: 1996-506148/50.
 XX N-PSDB: AAT45219.
 XX
 PT Use of extracellular Streptococcal cysteine protease enzyme - for
 PT inhibiting the proliferation of neoplastic cells, e.g. for treating
 PT carcinoma, lymphoma or leukemia.
 XX
 PS Disclosure: Pages 59-61; 99p; English.
 XX
 CC The present sequence is the Streptococcus pyogenes clone speB7
 CC pre-pro cysteine protease (CP), which can be used to inhibit
 CC neoplastic cell proliferation, especially in a human, useful in the
 CC treatment of neoplastic conditions, e.g. carcinomas, sarcomas,
 CC melanomas, lymphomas and leukemias originating from blood, lung,
 CC mammary gland, prostate, intestine, stomach, liver, heart, skin,
 CC pancreas or brain tissue. The CP is especially associated with a
 CC wound covering, and can also be used to prevent metastasis or
 CC identify susceptible neoplastic cells.
 CC K1735 and CHS19 melanoma cells were injected s.c. into nu/nu mice,
 CC optionally followed by i.p. injection of CP (100 microg, 24 hours
 CC later). The mice were checked twice weekly for tumour growth for
 CC 12 weeks, to give results that showed that treatment with CP
 CC completely protected athymic mice against transplanted K1735
 CC melanoma growth, and protected 60% of the mice from developing
 CC CHS19 melanomas.
 CC
 XX
 SO Sequence 398 AA;
 Query Match 53.1%; Score 1327.5; DB 17; Length 398;
 Best Local Similarity 91.5%; Pred. No. 1.5e-99;
 Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;
 QY 192 FTGSKYIMTKDNETLDSNTOIEVLT---KQPVKSLDSKGIHNOGNPYLLRPVI 248
 DB 120 FMES-YVEQIKENKKLT-----TYAGTAETKQPVKSLDSKGIHNOGNPYLLRPVI 173
 QY 249 EKVPGEQSFVGOHAATGCVATATAQIMKYNHYPNKGIDYTYLLSSNNPFNNPKMLFA 308
 DB 174 EKVPGEQSFVGOHAATGCVATATAQIMKYNHYPNKGIDYTYLLSSNNPFNNPKMLFA 233
 QY 309 AISTROYNMNNILPTYSGRSNNOKMAISELMADVGISVMDYGPSSGSGSSRVQRAK 368
 DB 234 AISTROYNMNNILPTYSGRSNNOKMAISELMADVGISVMDYGPSSGSGSSRVQRAK 293
 QY 369 ENFGYNQSVHOINSDS-ODMEAQIDKELSONOPVYVG-GKVGGAHFIYDAGDGRNFY 426
 DB 294 ENFGYNQSVHOINSDSKQDMEAQIDKELSONOPVYVGKVGGAHFIYDAGDGRNFY 353
 QY 427 HVNMGWGVSDGFPRDLALNPALGTGGAGGFGNGYQSAVVG 468
 DB 354 HVNMGWGVSDGFPRDLALNPALGTGGAGGFGNGYQSAVVG 395
 RESULT 2
 AAR95856
 ID AAR95856 standard; Protein: 398 AA.
 XX
 AC AAR95856;
 XX
 DT 30-OCT-1996 (first entry)
 XX
 DE S. pyogenes speB gene encoded extracellular protease.
 XX
 KW Immunogenic peptide; speB gene; extracellular protease; production;
 KW antibody; vaccine; diagnosis; detection; Streptococcus infection;
 KW group A; prevention; treatment; pharyngitis; tonsillitis;
 KW skin infection; acute rheumatic fever; scarlet fever; probe;
 KW post-streptococcal glomerulonephritis; sepsis; meningitis;
 KW erysipelas; cellulitis; fasciitis; toxic shock like syndrome.

XX
 OS Streptococcus pyogenes.
 XX
 FH Key Location/Qualifiers
 XX Domain 333..338
 FT Region /label= putative nucleotide binding domain
 FT Region 382..398
 FT Misc-difference 216
 FT /label= potential collagen docking region
 FT /note= "corresponding codon TAG"
 XX
 PN MO9608569-A2.
 XX
 PD 21-MAR-1996.
 XX
 XX 13-SEP-1995; 95WO-US11723.
 XX
 PR 14-SEP-1994; 94US-0306542.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Kapur V, Musser JA;
 XX
 DR WPI: 1996-179944/18.
 XX N-PSDB: AAT15294.
 XX
 PT Use of extracellular protease(s), partic. cysteine protease - for
 PT detection, diagnosis prevention and treatment of infection by
 PT pathogenic organisms, partic. gp. A streptococcus strains
 XX
 PS Disclosure: Page 12; 97p; English.
 XX
 CC The present sequence is the S. pyogenes speB gene encoded
 CC extracellular protease. An immunogenic peptide derived from the
 CC protease can be used in the prodn. of antibody (Ab) and vaccine. Ab
 CC is prepd. by introducing the peptide into a mammal, pref. a mouse,
 CC followed by Ab isolation. The Ab or a probe derived from the gene
 CC can be used for the diagnosis and detection of gp. A Streptococcus
 CC infections, while vaccine, which inhibits streptococcal
 CC replication, can be used to prevent and treat gp. A Streptococcus
 CC infections, and partic. to ameliorate pharyngitis, tonsillitis,
 CC skin infections, acute rheumatic fever, scarlet fever,
 CC post-streptococcal glomerulonephritis, sepsis, meningitis,
 CC erysipelas, cellulitis, fasciitis and toxic shock like syndrome.
 CC
 XX
 SO Sequence 398 AA;
 Query Match 53.1%; Score 1327.5; DB 17; Length 398;
 Best Local Similarity 91.5%; Pred. No. 1.5e-99;
 Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;
 QY 192 FTGSKYIMTKDNETLDSNTOIEVLT---KQPVKSLDSKGIHNOGNPYLLRPVI 248
 DB 120 FMES-YVEQIKENKKLT-----TYAGTAETKQPVKSLDSKGIHNOGNPYLLRPVI 173
 QY 249 EKVPGEQSFVGOHAATGCVATATAQIMKYNHYPNKGIDYTYLLSSNNPFNNPKMLFA 308
 DB 174 EKVPGEQSFVGOHAATGCVATATAQIMKYNHYPNKGIDYTYLLSSNNPFNNPKMLFA 233
 QY 309 AISTROYNMNNILPTYSGRSNNOKMAISELMADVGISVMDYGPSSGSGSSRVQRAK 368
 DB 234 AISTROYNMNNILPTYSGRSNNOKMAISELMADVGISVMDYGPSSGSGSSRVQRAK 293
 QY 369 ENFGYNQSVHOINSDS-ODMEAQIDKELSONOPVYVG-GKVGGAHFIYDAGDGRNFY 426
 DB 294 ENFGYNQSVHOINSDSKQDMEAQIDKELSONOPVYVGKVGGAHFIYDAGDGRNFY 353
 QY 427 HVNMGWGVSDGFPRDLALNPALGTGGAGGFGNGYQSAVVG 468
 DB 354 HVNMGWGVSDGFPRDLALNPALGTGGAGGFGNGYQSAVVG 395
 RESULT 3

AAV81812
 ID AAV81812 standard; Protein; 398 AA.
 AC AAV81812;
 XX
 XX
 DT 09-JUN-2000 (first entry)
 XX
 XX
 DE 5. pyogenes cysteine protease speB7 protein sequence.
 XX
 XX Cysteine protease; speB; Group A Streptococcus; extracellular protease;
 KW detection; diagnosis; extracellular matrix; infection; skin infection;
 KW disease status monitoring; vaccine; Streptococcus mediated disease;
 KW pharyngitis; tonsillitis; scarlet fever; sepsis; erysipelas; fasciitis;
 KW pneumonia; acute rheumatic fever; poststreptococcal glomerulonephritis;
 KW cellulitis; bacteraemia; meningitis.
 XX
 XX Streptococcus pyogenes.
 OS
 XX
 XX US6030835-A.
 PN
 XX
 XX 29-FEB-2000.
 PD
 XX
 XX 16-SEP-1997; 97US-0931220.
 PF
 XX
 XX 02-DEC-1993; 93US-0160965.
 PR
 XX 14-SEP-1994; 94US-0306542.
 XX
 XX (BAYU) BAYLOR COLLEGE MEDICINE.
 PA
 XX
 PI Kapur V, Musser JM;
 DR WPI: 2000-205208/18.
 DR N-PSDB; AAA07111.
 XX
 XX
 PT Determining the presence of a Group A Streptococcus expressing a
 PT protease capable of degrading proteins of the extracellular matrix,
 PT using a specific antibody.
 PT
 XX
 XX Disclosure: Column 7-8; 56pp; English.
 PS
 XX
 XX This sequence represents the S. pyogenes cysteine protease speB7.
 CC The invention relates to a method for determining the presence of a
 CC Group A Streptococcus which expresses an extracellular protease
 CC (preferably speB) capable of degrading proteins of the extracellular
 CC matrix, comprising: (1) combining a sample with an assay medium
 CC comprising a first member of a specific binding pair which binds to a
 CC second member of the binding pair to form a complex, where the first
 CC member has at least 1 epitopic site competitive with at least 1 conserved
 CC epitopic site on the protease; and (2) detecting complex formation as
 CC indicative of the presence of the pathogenic organism. The method is
 CC useful for screening host samples for evidence of infection with
 CC Streptococcus pyogenes and for monitoring the disease status of the host.
 CC The speB gene products are used as a vaccine for protecting against
 CC Streptococcus mediated diseases such as pharyngitis, tonsillitis,
 CC skin infections, scarlet fever, sepsis, erysipelas, fasciitis, pneumonia,
 CC acute rheumatic fever, poststreptococcal glomerulonephritis, cellulitis,
 CC bacteraemia, and meningitis.
 CC
 XX
 XX Sequence 398 AA;
 SQ
 Query Match 53.1%; Score 1327.5; DB 21; Length 398;
 Best Local Similarity 91.5%; Pred. No. 1.5e-99;
 Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;
 OY 192 FTQSKYLMYKDNEDTIDNSNTQIEVYLT--KQPVKSLDSKGIHYNOGNPNYNTLPVI 248
 DB 120 FMES-YVQIKENKLTDF-----YTAGTAETKQPVKSLDSKGIHYNOGNPNYNTLPVI 173
 OY 249 EKVVRGEQSFVGOHAATGCATATAQAQIMKYHNPKNKGLKDYTYTLLSSNNPFNHPKNLFA 308
 DB 174 EKVVRGEQSFVGOHAATGCATATAQAQIMKYHNPKNKGLKDYTYTLLSSNNPFNHPKNLFA 233
 OY 309 AISTROYMWNNTLPIYSGRESNVQKMAISELMADYGVISVDMDYGPSSGSSAGSSRYQRLAK 368

DB 234 AISTROYMWNNTLPIYSGRESNVQKMAISELMADYGVISVDMDYGPSSGSSAGSSRYQRLAK 293
 OY 369 ENFGTNSVHQINRSDFS-QDWEAOTIDKELSONQPVYIOG-GKVGHAVIDGADGRNFY 426
 DB 294 ENFGTNSVHQINRSDFSQDWEAOTIDKELSONQPVYIOGVKVGHAVIDGADGRNFY 353
 OY 427 HYNMGMGVSDGFFRLDALNPALCTGGAGGFGNQSAYVG 468
 DB 354 HYNMGMGVSDGFFRLDALNPALCTGGAGGFGNQSAYVG 395
 RESULT 4
 ID AAV81812 standard; Protein; 398 AA.
 AC AAV81812;
 XX
 XX
 DT 02-JUL-2002 (first entry)
 XX
 XX Streptococcus polypeptide SEQ ID NO 8334.
 DE
 XX
 XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX
 XX Streptococcus pyogenes.
 OS
 XX
 XX WO200234771-A2.
 PN
 XX
 XX 02-MAY-2002.
 PD
 XX
 XX 29-OCT-2001; 2001WO-GB04789.
 PF
 XX
 XX 27-OCT-2000; 2000GB-0026333.
 PR
 XX 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX
 XX
 XX (CHTR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 XX Telford J, Maignan V, Margalit Ros YI, Grandi G, Fraser C;
 PI Telford J;
 PI
 XX
 XX WPI: 2002-352536/38.
 DR N-PSDB; AEN70210.
 DR
 XX
 XX New Streptococcus protein for the treatment or prevention of infection
 XX or disease caused by Streptococcus bacteria, such as meningitis, and
 XX for detecting a compound that binds to the protein -
 XX
 XX Claim 1; Page 3948; 4525pp; English.
 PS
 XX
 XX The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.
 CC
 XX
 XX Sequence 398 AA;
 SQ

Query Match 52.9% Score 1323.5: DB 23; Length 398;
Best Local Similarity 91.1%: Pred. No. 3.2e-99;
Matches 257; Conservative 5; Mismatches 9; Indels 11; Gaps 5

QY 192 FTOSKYLIIIVYKDNEDTINSDNTQIEVYLT---KQPVKSLDLSKGIHYNQGNFYNLLTPVI 248
DB 120 FMES-YVBOIKENKKLDT-----YAGIAEIKQPVKSLDLSKGIHYNQGNFYNLLTPVI 173
QY 249 EKVAFGEOSFVGQHAATCCVATATPQIKYHYNPVKGLKDYTYLLSSNNPFNHPKNTFA 308
DB 174 EKVKGESFVGQHAATCCVATATPQIKYHYNPVKGLKDYTYLLSSNNPFNHPKNTFA 233
QY 309 AISTROYMNNILTPYSGRESNVOKMAISELMADVGISVMDYDGPSSGAGSSRYORALK 368
DB 224 AISTROYMNNILTPYSGRESNVOKMAISELMADVGISVMDYDGPSSGAGSSRYORALK 293
QY 369 ENFGYNSVHOINRSDFS-QDWEAQIDELSONQPVYTG-QKVGSHAFVIDGADGRNFY 426
DB 294 ENFGYNSVHOINRDFSPKQDEAQIDELSONQPVYTGQKVGSHAFVIDGADGRNFY 353
QY 427 HVMNGMGVSDGFFFRDLALNPSALCTGGAGGFNGYQSAVVG 468
DB 354 HVMNGMGVSDGFFFRDLALNPSALCTGGAGGFNGYQSAVVG 395

RESULT 5
AAB36098
ID AAB36098 standard; Protein; 398 AA.
AC AAB36098;
XX
XX
DT 16-FEB-2001 (first entry)
XX
DE Streptococcus pyogenes streptocain.
XX
KM Streptococcus pyogenes; streptocain; periodontain; antiinflammatory;
XX antibacterial; amidolytic; alpha_1-proteinase inhibitor; periodontitis;
KM gingivitis.
XX
OS Streptococcus pyogenes.
XX
PN WO20063394-A2.
XX
PD 26-OCT-2000.
XX
PF 20-APR-2000; 2000WO-US10574.
XX
PR 21-APR-1999; 99US-0130436.
XX
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
PA (TRAV/) TRAVIS J.
PA (POTE/) POTEPA J.
PA (NELS/) NELSON D.
XX
PI Travis J, Potempa J, Nelson D;
XX
XX WPI: 2000-679600/66.
XX
XX
XX Novel oral bacteroid periodontain polyepitope for treating periodontal
PT diseases, has amidolytic activity for cleavage of non-denatured human
PT alpha1-proteinase inhibitor at reactive site loop region of inhibitor
PT
XX
XX
XX Example 1: Fig 1: 55pp; English.
XX
XX The present sequence is given in a specification relating to novel
CC oral bacterial polypeptide referred to as periodontain. The polypeptide
CC has amidolytic activity for cleavage of denatured polypeptides and
CC non-denatured serpin polypeptides. It has amidolytic activity for
CC cleavage of a non-denatured human alpha_1-proteinase inhibitor at a
CC reactive site loop region of the inhibitor. Periodontain is useful for
CC inhibiting the peptidase activity and reducing periodontitis, loss of
CC tooth attachment and periodontal pocket formation, and for reducing

growth of bacteria, preferably P. gingivalis in vitro or in vivo.
It is useful for protecting an animal from a disease caused by
P. gingivalis and for treating periodontal diseases, including
gingivitis and periodontitis.

Sequence 398 AA;

Query Match 47.8%; Score 1195.5; DB 21; Length 398;
Best Local Similarity 84.0%; Pred. No. 6,2e-85;
Matches 237; Conservative 5; Mismatches 29; Indels 11; Gaps 5;

OY 192 FTQSKYLIVADNDELSTNFQIEVYLT---KQPVKSLDSKGIHNOGNPNLTPVI 248
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 120 FMES-YVEQIKENKLDP-----TYAGIAELKQXVKXSLLDSKIHNOGNPNLTPXX 173

OY 249 EKVPFEGSEFVGQAHAATGCVAATAAQLMKYHNYPNGKLKDYTYTLSSNNPFNHPPKNLFA 308
EKVPFEGSEFVGQAHAATGCVAATAAQLMKYHNYPNGKLKDYTYTLSSNNPFNHPPKNLXX 233

Db 174 EKVPFEGSEFVGQAHAATGCVAATAAQLMKYHNYPNGKLKDYTYTLSSNNPFNHPPKNLXX 233

OY 309 AISTROYMWNILPTYSGRESNVOKMAISELMADVGSVDMDPYRSGSAGSSRYORALK 368
AISTROYMWNILPTYSGRESNVOKMAISELMADVGSVDMDXXPSGSAASSRYORALX 293

Db 369 ENFGNOSVHOINRSD-FSQDMEAQIDKELSQNOPYYG-GKYGGHAFVIDGAGRNFY 426
ENFGNOSVHOINRSDFKQDMEOIDKELSQNOPYYGCKYGGHAFVIDGAGRNFEX 353

OY 427 HYNMGWGVSDGFPRDLALNPALGTGGAGGFGNGOAVVG 468
HYNMGWGVSDGFPRDLALNPALGTGGAGGFGNGOAVVG 395

Db 354 HYNMGWGVSDGFPRDLALNPALGTGGAGGFGNGOAVVG 395

RESULT 6
AAAY70109
ID AAAY70109 standard; Protein: 251 AA.
AC AAAY70109;
DT 05-JUN-2000 (first entry)
DE Streptococcus pyrogenic exotoxin A (SPE-A).
KM Superantigen toxin; SAg; Streptococcus pyrogenic exotoxin A; SPE-A;
KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
KM cytostatic; antibody; staphylococcal/streptococcal toxin; Toxoid; SPEA42;
diagnosis; treatment; superantigen-associated bacterial infection.
XX Streptococcus sp.
OS
XX
XX WO200009154-A1.
PM
XX
XX 24-FEB-2000.
PD
XX
XX 13-AUG-1998; 98WO-US16766.
PF
XX
XX 13-AUG-1998; 98WO-US16766.
PR
XX
XX (REED-) REED ARMY INST RES WALTER.
PA
XX
XX Ulrich RG, Olson MA, Bavari S;
PI
XX
XX WPI: 2000-224177/19.
DR N-PSDB: AA251112.
XX
XX Nucleic acid encoding superantigen toxin useful as a vaccine and for
PT diagnosis of superantigen-associated bacterial infections -
PS Example 12; Page 94-95; 118pp; English.
XX
XX The present amino acid sequence is the streptococcal pyrogenic
CC exotoxin A (SPE-A), a bacterial superantigen toxin (SAg), used for the
CC formulation of SPE-A vaccine SPEA42. The coding region of this SAg toxin
CC is altered by site directed mutagenesis, introducing L42Z mutation, that

CC results in disruption of binding of the toxin to both the MHC class II
 CC or T-cell antigen receptor. SPE-A has antibacterial and cytostatic
 CC activity. This sequence is useful for the production of SPE-A vaccines
 CC and specific antibodies. This vaccine overcomes the disadvantages of the
 CC chemically inactivated toxoids and is designed to protect individuals
 CC against one or several related staphylococcal and streptococcal toxins.
 CC It is used for the diagnosis and treatment or amelioration of
 CC superantigen-associated bacterial infections.

XX Sequence 251 AA;

Query Match 45.4%; Score 1136; DB 21; Length 251;
 Best Local Similarity 98.2%; Pred. No. 3e-84;
 Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY 2 QDDPDSQHRSSLVNNDNIYFLYEGDPVTHNVKSVQQLRSHDLIYVSGPNYDKLT 61
 DB 31 QDDPDSQHRSSLVNNDNIYFLYEGDPVTHNVKSVQQLRSHDLIYVSGPNYDKLT 90
 QY 62 ELKNQEMATLFDKNDIYGVYHLCYLCENNAERSACI-GGYTNRGNHLEIPKRIYK 120
 DB 91 ELKNQEMATLFDKNDIYGVYHLCYLCENNAERSACIYGVYTNHGNHLEIPKRIYK 150
 QY 121 VSIDGIQSLSFDIETNKKKWTAGQELDYKVRKYLTDNKKQLYTNGPSKYEYGIKFIKPKNE 180
 DB 151 VSIDGIQSLSFDIETNKKKWTAGQELDYKVRKYLTDNKKQLYTNGPSKYEYGIKFIKPKNE 210
 QY 181 SFWFDFPEPEFTQSKYLMITKDNETLDSNT-QIEVYLTK 220
 DB 211 SFWFDFPEPEFTQSKYLMITKDNETLDSNTQIEVYLTK 251

RESULT 7

ABB79508
 ID ABB79508 standard; Protein; 251 AA.

XX ABB79508;

XX 23-SEP-2002 (first entry)

DE Streptococcal pyrogenic exotoxin A vaccine SPEA42.

XX Exotoxin A; SPEA; SPEA42; superantigen; antigen; toxin; vaccine;
 KW attenuation; mutant; mutelin.

OS Streptococcus pyogenes.

XX Synthetic.

XX US6399332-B1.

XX 04-JUN-2002.

XX 01-SEP-1998; 98US-0144776.

XX 25-JUN-1997; 97US-0882431.

XX (USSA) US SEC OF ARMY.

XX Ulrich RG, Olson MA, Bavari S;

XX WPI; 2002-546281/58.

XX N-PSDB; ABBN84229.

PT Novel isolated and purified superantigen toxin DNA fragment which has
 PT been genetically altered, useful for producing vaccine for treatment of
 PT superantigen toxin-associated bacterial diseases

XX Disclosure; Column 63-65; 46pp; English.

XX The present sequence is the protein sequence of Streptococcus
 CC pyogenes vaccine SPEA42. The vaccine differs from the native SPEA
 CC sequence by substitution of the Leu-42 residue by Arg. This
 CC mutation is expected to disrupt contact between the toxin and the

CC HLA-DR receptor, reducing DR1 binding. SPEA42 can be expressed as
 CC a recombinant protein in Escherichia coli as a secreted protein or
 CC as a cytoplasmic product. No indicators of toxicity have been
 CC detected for the purified recombinant protein, and vaccine studies
 CC demonstrate that SPEA42 is highly antigenic, inducing protective
 CC immunity in a mouse animal model. The attenuated superantigen can
 CC be used to protect against superantigen toxin infections. Methods of
 CC producing and using altered superantigen toxins as vaccines, and in
 CC diagnosis and therapy, are provided by the invention. A multivalent
 CC vaccine consisting of altered superantigen toxins from SEA, SEB,
 CC SEC-1, TSSr-1 and SPEA is predicted to provide protective immunity
 CC against the majority of bacterial superantigen toxins.

XX Sequence 251 AA;

Query Match 45.4%; Score 1136; DB 23; Length 251;
 Best Local Similarity 98.2%; Pred. No. 3e-84;
 Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY 2 QDDPDSQHRSSLVNNDNIYFLYEGDPVTHNVKSVQQLRSHDLIYVSGPNYDKLT 61
 DB 31 QDDPDSQHRSSLVNNDNIYFLYEGDPVTHNVKSVQQLRSHDLIYVSGPNYDKLT 90
 QY 62 ELKNQEMATLFDKNDIYGVYHLCYLCENNAERSACI-GGYTNRGNHLEIPKRIYK 120
 DB 91 ELKNQEMATLFDKNDIYGVYHLCYLCENNAERSACIYGVYTNHGNHLEIPKRIYK 150
 QY 121 VSIDGIQSLSFDIETNKKKWTAGQELDYKVRKYLTDNKKQLYTNGPSKYEYGIKFIKPKNE 180
 DB 151 VSIDGIQSLSFDIETNKKKWTAGQELDYKVRKYLTDNKKQLYTNGPSKYEYGIKFIKPKNE 210
 QY 181 SFWFDFPEPEFTQSKYLMITKDNETLDSNT-QIEVYLTK 220
 DB 211 SFWFDFPEPEFTQSKYLMITKDNETLDSNTQIEVYLTK 251

RESULT 8

ABB67344
 ID ABB67344 standard; peptide; 221 AA.

XX ABB67344;

XX 23-APR-2001 (first entry)

DE Streptococcus pyogenes toxin A protein.

XX Tumour; cancer; immune; enterotoxin.

XX Streptococcus pyogenes.

XX US6180097-B1.

XX 30-JAN-2001.

XX 30-OCT-1998; 98US-0183437.

XX 31-JAN-1994; 94US-0189424.

XX 19-JUN-1995; 95US-0491746.

XX 03-OCT-1989; 89US-0416530.

XX 17-JAN-1990; 90US-0466577.

XX 01-JUN-1992; 92US-0891718.

XX 02-MAR-1993; 93US-0025144.

XX (TERM/) TERMAN D S.

XX Terman DS;

XX WPI; 2001-158657/16.

PT Tumor cell capable of stimulating antitumor immune reactivity in vitro
 PT or in vivo complies exogenous nucleic acids encoding a superantigen
 PT and a costimulatory molecule

XX XX Disclosure; Fig 2; 16pp; English.
 PS XX
 CC CC The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and
 CC expresses an exogenous nucleic acid molecule encoding a superantigen
 CC or its active fragment and an exogenous nucleic acid molecule
 CC encoding a costimulatory molecule that activates T cells in
 CC conjunction with an antigenic stimulus. The invention may be used
 CC for cancer therapy by stimulating an anticancer immune response
 CC in vivo or ex vivo.
 CC XX
 SQ Sequence 221 AA;
 Query Match 45.2%; Score 1129; DB 22; Length 221;
 Best Local Similarity 97.7%; Pred. No. 9.2e-84;
 Matches 216; Conservative 1; Mismatches 2; Indels 2; Gaps 2;
 QY 2 QQDDPSPQLHRSLSLVKNIQNIYFLYEGDPYTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
 DB 1 QQDDPSPQLHRSLSLVKNIQNIYFLYEGDPYTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 60
 QY 62 ELKQEMATLFEKDNIDYGVYHYHLCYLCENARSACI-GGVYNRGSHLEIPKTIYVK 120
 DB 61 ELKQEMATLFEKDNIDYGVYHYHLCYLCENARSACI-GGVYNRGSHLEIPKTIYVK 120
 QY 121 VSIDGIQSLSPDIETNNKMYTAQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 180
 DB 121 VSIDGIQSLSPDIETNNKMYTAQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 180
 QY 181 SFWFDFPEPEFTOSKYLMIYKDNETLDSNT-QIEVYLTK 220
 DB 181 SFWFDFPEPEFTOSKYLMIYKDNETLDSNTQIEVYLTK 221

RESULT 9
 AAR13209
 ID AAR13209 standard; protein: 221 AA.
 AC AAR13209;
 XX
 DT 15-OCT-1991 (first entry)
 XX
 DE Streptococcal pyrogenic enterotoxin A.
 XX
 KW SPE A; cancer treatment; pyrogen; tumouricide; scarlet fever.
 XX
 OS Streptococcus NY-5 strain.
 XX
 PN W09110680-A.
 XX
 PD 25-JUL-1991.
 XX
 PF 17-JAN-1991; 91WO-US00342.
 XX
 PR 17-JAN-1990; 90US-0466577.
 XX
 PA (TERM/) TERNAN D S.
 XX
 PI Terman DS;
 XX
 DR WPI: 1991-237984/32.
 XX
 XX Treating cancer with enterotoxin from *Staphylococcus aureus* -
 PT administered by IV injection, having same tumouricidal activity
 PT as *Staphylococcal* protein A without potential toxic reactions
 XX
 PS Disclosure; Fig 1; 74pp; English.
 CC SPE A can be used for tumouricidal treatment, esp. with a haemolysin.
 CC Synthetic polypeptides having structural homology to Streptococcal
 CC pyrogenic exotoxins are claimed. provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine

CC residues and similar hydropathy profiles.
 CC See AAR13203-R13211.
 CC XX
 SQ Sequence 221 AA;
 Query Match 44.9%; Score 1123; DB 12; Length 221;
 Best Local Similarity 97.3%; Pred. No. 2.8e-83;
 Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;
 QY 2 QQDDPSPQLHRSLSLVKNIQNIYFLYEGDPYTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
 DB 1 QQDDPSPQLHRSLSLVKNIQNIYFLYEGDPYTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 60
 QY 62 ELKQEMATLFEKDNIDYGVYHYHLCYLCENARSACI-GGVYNRGSHLEIPKTIYVK 120
 DB 61 ELKQEMATLFEKDNIDYGVYHYHLCYLCENARSACI-GGVYNRGSHLEIPKTIYVK 120
 QY 121 VSIDGIQSLSPDIETNNKMYTAQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 180
 DB 121 VSIDGIQSLSPDIETNNKMYTAQELDYKVRKYLTDNKKQLYTNGPSKYETGYIKFIPKNKE 180
 QY 181 SFWFDFPEPEFTOSKYLMIYKDNETLDSNT-QIEVYLTK 220
 DB 181 SFWFDFPEPEFTOSKYLMIYKDNETLDSNTQIEVYLTK 221

RESULT 10
 AAR45017
 ID AAR45017 standard; protein: 221 AA.
 AC AAR45017;
 XX
 DT 08-JUN-1994 (first entry)
 XX
 DE *Staphylococcal* enterotoxin SPE A.
 XX
 KW *Staphylococcal* enterotoxin; SE; cancer; tumouricidal agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.
 XX
 OS *Staphylococcus aureus*.
 XX
 PN W09324136-A.
 XX
 PD 09-DEC-1993.
 XX
 PF 01-JUN-1993; 93WO-US05213.
 XX
 PR 01-JUN-1992; 92US-0891718.
 XX
 PA (STON/) STONE J L.
 XX
 PA (TERM/) TERNAN D S.
 XX
 PI Stone JL, Terman DS;
 XX
 DR WPI: 1993-405418/50.
 XX
 XX Use of *staphylococcal* enterotoxin(s) and homologues - for
 PT treating cancer in a patient or for the treatment of auto-immune
 PT diseases
 XX
 PS Disclosure; Fig 1; 90pp; English.
 CC The sequences given in AAR45011-21 are *Staphylococcal* enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer
 CC in a patient. These SEs, and homologues of them, can be used as
 CC tumouricidal agents for treating cancers and autoimmune disease.
 CC They exhibit tumouricidal activity and toxicity identical to that
 CC observed for the Protein A perfusion system. They may be administered
 CC by i.v. injection.
 CC XX
 SQ Sequence 221 AA;
 Query Match 44.9%; Score 1123; DB 14; Length 221;

Best Local Similarity 97.3%; Pred. No. 2,8e-83;
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

OY 2 QODPPESQHRSSLVKNLONIFLYEGDPVTHENKVSQVQLSHDLIYVSGPNRYKLT 61
DB 1 QODPPESQHRSSLVKNLONIFLYEGDPVTHENKVSQVQLSHDLIYVSGPNRYKLT 60
OY 62 ELKNQEMATLFRKNDIYGVGYHLCYCENASRSACI-GGVYTRNGNHLLEIPKRIYK 120
DB 61 ELKNQEMATLFRKNDIYGVGYHLCYCENASRSACIYGVYTRNGNHLLEIPKRIYK 120
OY 121 VSIDGIQSLSFDIETNKKMVTAGQELDYKVRKYLTDNKKQLYTNGPSKYEYGIKFIKPKNE 180
DB 121 VSIDGIQSLSFDIETNKKMVTAGQELDYKVRKYLTDNKKQLYTNGPSKYEYGIKFIKPKNE 180
OY 181 SFWFDFPEPEPTQSKYLMYKDNFTLDSNT-QIEVYLLTK 220
DB 181 SFWFDFPEPEPTQSKYLMYKDNFTLDSNTQIEVYLLTK 221

RESULT 11

ID ABB76240 standard; Protein; 221 AA.

XX ABB76240;

DT 09-AUG-2002 (first entry)

DE Staphylococcus pyogenes exotoxin A.

KW Exotoxin A; SPE A; superantigen; antigen; tumour; cancer;
antitumour; therapy.

OS Streptococcus pyogenes.

PN US2002051765-A1.

PD 02-MAY-2002.

PF 19-DEC-2000; 2000US-0741503.

PR 31-JAN-1994; 94US-0189424.

PR 19-JUN-1995; 95US-0491746.

PR 03-OCT-1989; 89US-0416530.

PR 17-JAN-1990; 90US-0466577.

PR 01-JUN-1992; 92US-0891718.

PR 02-MAR-1993; 93US-0025144.

PA (TERM/) TERMAN D S.

PI Terman DS;

DR WPI: 2002-415198/44.

PT Reagent for treating cancer without the need for e.g. radiotherapy,
comprises a specific V beta subset of T cells sensitized to a growing
tumour and stimulated with superantigens

PS Disclosure; Fig 2; 17pp; English.

XX The present sequence is the protein sequence of exotoxin A (SPE A)

CC of Streptococcus pyogenes. Similarity is shown, in several

CC stretches of sequence, between staphylococcal enterotoxins,

CC streptococcal pyrogenic exotoxins and staphylococcal exfoliative

CC toxins (see ABB76234-44). In the present invention, synthetic

CC polypeptides useful in tumour therapy and in blocking or destroying

CC autophagocytosis and B lymphocyte populations are characterised by

CC substantial structural homology to staphylococcal enterotoxin A and

CC enterotoxin B, and to streptococcal pyrogenic exotoxins, with

CC statistically significant sequence homology and similarity (2 value

CC of Lipman and Pearson algorithm in Monte Carlo analysis exceeding

CC 6) to include alignment of cysteine residues and similar hydrophathy

CC profiles. These superantigens are used to treat solid tumours,
CC including their metastases, without radiation, surgery or
CC standard chemotherapeutic agents. A claimed method of human cancer
CC treatment involves contacting haematopoietic cells from a patient
CC with one or more superantigens ex vivo to generate stimulated cells,
CC selecting a specific V beta subset of cells, and reintroducing
CC these cells into the patient to induce an in vivo therapeutic,
CC tumouricidal reaction.

SO Sequence 221 AA;

Query Match 44.9%; Score 1123; DB 23; Length 221;

Best Local Similarity 97.3%; Pred. No. 2,8e-83;

Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

OY 2 QODPPESQHRSSLVKNLONIFLYEGDPVTHENKVSQVQLSHDLIYVSGPNRYKLT 61
DB 1 QODPPESQHRSSLVKNLONIFLYEGDPVTHENKVSQVQLSHDLIYVSGPNRYKLT 60
OY 62 ELKNQEMATLFRKNDIYGVGYHLCYCENASRSACI-GGVYTRNGNHLLEIPKRIYK 120
DB 61 ELKNQEMATLFRKNDIYGVGYHLCYCENASRSACIYGVYTRNGNHLLEIPKRIYK 120
OY 121 VSIDGIQSLSFDIETNKKMVTAGQELDYKVRKYLTDNKKQLYTNGPSKYEYGIKFIKPKNE 180
DB 121 VSIDGIQSLSFDIETNKKMVTAGQELDYKVRKYLTDNKKQLYTNGPSKYEYGIKFIKPKNE 180
OY 181 SFWFDFPEPEPTQSKYLMYKDNFTLDSNT-QIEVYLLTK 220
DB 181 SFWFDFPEPEPTQSKYLMYKDNFTLDSNTQIEVYLLTK 221

RESULT 12

ID AAM12097 standard; Protein; 251 AA.

XX AAM12097;

DT 04-NOV-1997 (first entry)

DE Streptococcus pyogenes Streptococcal toxin A.

KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;

KW vaccine; protection; treatment; cancer; neutralising antibody;

KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;

KW fever; hypotension; group A streptococcal infection; myositis;

KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.

OS Streptococcus pyogenes.

FT Key Location/Qualifiers

FT Peptide 1..30 /label= sig_peptide

FT Peptide 31..251 /label= mat_peptide

PD 19-DEC-1996.

PF 07-JUN-1996; 96MO-US10252.

PR 07-JUN-1995; 95US-0480261.

PA (MINT) UNIV MINNESOTA.

PI Ohlendorf D, Roggiani M, Schlievert PM, Stoeckl J;

DR N-PSDB; AAM12097.

PT Mutant SPE-A toxin with at least one amino acid change is
substantially non-lethal - used in vaccine composition for

PT treatment of cancer and streptococcal toxic shock syndrome etc.
XX
PS Disclosure: Pages 77-79; 102pp; English.
XX

CC The present sequence is Streptococcus pyogenes Streptococcal
CC toxin A (SPE-A), from which a non-lethal mutant SPE-A, comprising
CC at least 1 amino acid change, can be derived. The mutant SPE-A can
CC be used to produce vaccines to protect animals against wild type
CC SPE-A and to treat cancer and streptococcal toxic shock syndrome
CC (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be
CC produced, which may be used to ameliorate STSS symptoms, e.g.
CC fever, hypotension, group A streptococcal infection, myositis,
CC fasciitis and liver damage. The neutralising Ab is preferably
CC administered in conjunction with antibiotic therapy. The mutant
CC SPE-A is especially useful for treating T cell lymphomas, and
CC ovarian and uterine cancer. It is thought that mutant SPE-A can be
CC selectively toxic to T cell lymphoma cells.
CC
XX

Sequence 251 AA;

Query Match 44.9%; Score 1122; DB 18; Length 251;
Best Local Similarity 97.3%; Pred. No. 4.1e-83;
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

QY 2 QQDDPSPQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSYDQLRSHDLIYNVSGPNYDKLKT 61
DB 31 QQDDPSPQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSYDQLRSHDLIYNVSGPNYDKLKT 90
QY 62 ELKQENMALTLEKDNIDIVGYEYHLCYLCEAERSACT-GGVNREGNHLIEIPKTIYVK 120
DB 91 ELKQENMALTLEKDNIDIVGYEYHLCYLCEAERSACTIGGVNREGNHLIEIPKTIYVK 150
QY 121 VSIDGIGSLSDIETNKKMWTAGLDYKVRKYLTNDNOLYNGPSKYETGYIKRIPKNKE 180
DB 151 VSIDGIGSLSDIETNKKMWTAGLDYKVRKYLTNDNOLYNGPSKYETGYIKRIPKNKE 210
QY 181 SFWDFPEPEPEFTQSKYLMYKDNETLDSNT-QIEVYLTKR 220
DB 211 SFWDFPEPEPEFTQSKYLMYKDNETLDSNTSQIEVYLTKR 251

RESULT 13
AAW59780
ID AAW59780 standard; Protein: 251 AA.
XX
AC AAW59780;
XX
DT 12-OCT-1998 (first entry)
XX

DE Amino acid sequence of Streptococcus pyogenes exotoxin A.

XX SPE-A toxin; nonlethal; mutant; Streptococcus pyogenes exotoxin A;
KW wild type; nontoxic; antibody; vaccine; immunity; ovarian cancer;
KW streptococcal toxic shock syndrome; STSS; T cell lymphoma;
KW uterine cancer.
XX

OS Streptococcus pyogenes.

XX WO9824911-A2.

XX 11-JUN-1998.

XX 05-DEC-1997; 97WO-US22228.

XX 06-DEC-1996; 96US-0032930.

XX (MINU) UNIV MINNESOTA.

XX Ohlendorf D, Roggiani M, Schlievert PM, Stoeckl J;
XX
XX WPI; 1998-333330/29.
XX
XX N-PSDB; AAWA1593.
XX

PT New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention
XX or treatment of streptococcal infection or toxic shock syndrome
XX
PS Disclosure: Fig 3; 95pp; English.
XX

CC This is the amino acid sequence of the Streptococcus pyogenes exotoxin A
CC (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin has at least
CC 1 aa change and is nonlethal compared with a protein to wild type SPE-A
CC toxin. The mutant SPE-A toxins are nontoxic and can produce antibodies
CC that neutralise wild type SPE-A toxin activity. The toxins can be used
CC in vaccines and therapeutics to generate a protective immune response
CC against streptococcal infection. They can be used to protect against the
CC development of streptococcal toxic shock syndrome (STSS). In addition,
CC the toxins can be used for treating animals with symptoms of
CC streptococcal infection or STSS and in methods for stimulating T cell
CC proliferation and in the treatment of cancer. In particular they can be
CC used for treating T cell lymphomas, and ovarian and uterine cancer.
CC
XX

Sequence 251 AA;

Query Match 44.9%; Score 1122; DB 19; Length 251;
Best Local Similarity 97.3%; Pred. No. 4.1e-83;
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

QY 2 QQDDPSPQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSYDQLRSHDLIYNVSGPNYDKLKT 61
DB 31 QQDDPSPQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSYDQLRSHDLIYNVSGPNYDKLKT 90
QY 62 ELKQENMALTLEKDNIDIVGYEYHLCYLCEAERSACT-GGVNREGNHLIEIPKTIYVK 120
DB 91 ELKQENMALTLEKDNIDIVGYEYHLCYLCEAERSACTIGGVNREGNHLIEIPKTIYVK 150
QY 121 VSIDGIGSLSDIETNKKMWTAGLDYKVRKYLTNDNOLYNGPSKYETGYIKRIPKNKE 180
DB 151 VSIDGIGSLSDIETNKKMWTAGLDYKVRKYLTNDNOLYNGPSKYETGYIKRIPKNKE 210
QY 181 SFWDFPEPEPEFTQSKYLMYKDNETLDSNT-QIEVYLTKR 220
DB 211 SFWDFPEPEPEFTQSKYLMYKDNETLDSNTSQIEVYLTKR 251

RESULT 14
AAW12154
ID AAW12154 standard; Protein: 251 AA.
XX
AC AAW12154;
XX

DT 04-NOV-1997 (first entry)
XX

DE Streptococcus pyogenes Streptococcal toxin A mutant Ser195Aa.

XX Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
KW vaccine; protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
KW fever; hypotension; group A streptococcal infection; myositis;
KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
XX

OS Streptococcus pyogenes.

XX Synthetic.

XX Key Location/Qualifiers

XX Peptide 1..30 /label= sig-peptide

XX Peptide 31..251 /label= mat-peptide

XX Misc-difference 225 /note= "wild type Ser replaced by Ala"

XX WO9640930-A1.

XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US10252.
XX

XX 07-JUN-1995: 95US-0480261.
XX (MINU) UNIV MINNESOTA.
XX Ohlendorf D, Roggliani M, Schlievert PM, Stoehr J;
XX WPI: 1997-099936/09.
XX
XX Mutant SPE-A toxin with at least one amino acid change is
XX substantially non-lethal - used in vaccine composition for
XX treatment of cancer and streptococcal toxic shock syndrome etc.
XX
XX Example 4; Page -: 102pp; English.
XX
XX The present sequence is a non-lethal Streptococcus pyogenes
XX Streptococcal toxin A (SPE-A) mutant, which can be used to produce
XX vaccines to protect animals against wild type SPE-A and to treat
XX cancer and streptococcal toxic shock syndrome (STSS). The mutant
XX SPE-A causes neutralising antibodies (Ab) to be produced, which
XX may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
XX group A streptococcal infection, myositis, fasciitis and liver
XX damage. The neutralising Ab is preferably administered in
XX conjunction with antibiotic therapy. The mutant SPE-A is
XX especially useful for treating T cell lymphomas, and ovarian and
XX uterine cancer. It is thought that mutant SPE-A can be selectively
XX toxic to T cell lymphoma cells.
XX N.B. Sequence not given in the specification, but constructed
XX using the wild type SPE-A sequence given on pages 77-79.
XX
SQ Sequence 251 AA:
Query Match 44.8%; Score 1119; DB 18; Length 251;
Best Local Similarity 96.8%; Pred. No. 7.2e-83;
Matches 214; Conservative 2; Mismatches 3; Indels 2; Gaps 2;
QY 2 QODPPSQLHRSLSLVKNLONIYFLYEGDPVTHENKSVQDLRSHDLIYVNSGPNYDKLT 61
DB 31 QODPPSQLHRSLSLVKNLONIYFLYEGDPVTHENKSVQDLRSHDLIYVNSGPNYDKLT 90
QY 62 ELKNOEMATLFDKNDIDIVGEVYHLCYCENASERSACI-GGVNREGNHLLEIPKRIYVK 120
DB 91 ELKNOEMATLFDKNDIDIVGEVYHLCYCENASERSACI-GGVNREGNHLLEIPKRIYVK 150
QY 121 VSIDGIQSLSFDIETNKKMVTAEQELDYKRYKYLTDNKQLYTGSPSYETGYIKFIIPKNE 180
DB 151 VSIDGIQSLSFDIETNKKMVTAEQELDYKRYKYLTDNKQLYTGSPSYETGYIKFIIPKNE 210
QY 181 SFWFDFPEPEPTQSKYLMIVKDNFTLDSNT-QIEVYLYTK 220
DB 211 SFWFDFPEPEPTQSKYLMIVKDNFTLDSNTQIEVYLYTK 251

RESULT 15
AAW12146
ID AAW12146 standard; Protein; 251 AA.
XX
XX AAW12146;
XX
XX 04-NOV-1997 (first entry)
XX
XX Streptococcus pyogenes Streptococcal toxin A mutant Lys157Glu.
XX
XX Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
XX vaccine; protection; treatment; cancer; neutralising antibody;
XX streptococcal toxic shock syndrome; STSS; symptom; amelioration;
XX fever; hypotension; group A streptococcal infection; myositis;
XX fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
XX
XX Streptococcus pyogenes.
XX Synthetic.
XX
XX Key Location/Qualifiers
FH

FT Peptide 1..30
FT /label= sig_peptide
FT Reptide 31..251
FT /label= mat_peptide
FT Misc-difference 187
FT /note= "wild type Lys replaced by Glu"
XX
XX MO9640930-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US10252.
XX
XX 07-JUN-1995; 95US-0480261.
XX
XX (MINU) UNIV MINNESOTA.
XX
XX Ohlendorf D, Roggliani M, Schlievert PM, Stoehr J;
XX WPI: 1997-099936/09.
XX
XX Mutant SPE-A toxin with at least one amino acid change is
XX substantially non-lethal - used in vaccine composition for
XX treatment of cancer and streptococcal toxic shock syndrome etc.
XX
XX Claim 5; Page -: 102pp; English.
XX
XX The present sequence is a non-lethal Streptococcus pyogenes
XX Streptococcal toxin A (SPE-A) mutant, which can be used to produce
XX vaccines to protect animals against wild type SPE-A and to treat
XX cancer and streptococcal toxic shock syndrome (STSS). The mutant
XX SPE-A causes neutralising antibodies (Ab) to be produced, which
XX may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
XX group A streptococcal infection, myositis, fasciitis and liver
XX damage. The neutralising Ab is preferably administered in
XX conjunction with antibiotic therapy. The mutant SPE-A is
XX especially useful for treating T cell lymphomas, and ovarian and
XX uterine cancer. It is thought that mutant SPE-A can be selectively
XX toxic to T cell lymphoma cells.
XX N.B. Sequence not given in the specification, but constructed
XX using the wild type SPE-A sequence given on pages 77-79.
XX
SQ Sequence 251 AA:
Query Match 44.7%; Score 1118; DB 18; Length 251;
Best Local Similarity 96.8%; Pred. No. 8.7e-83;
Matches 214; Conservative 2; Mismatches 3; Indels 2; Gaps 2;
QY 2 QODPPSQLHRSLSLVKNLONIYFLYEGDPVTHENKSVQDLRSHDLIYVNSGPNYDKLT 61
DB 31 QODPPSQLHRSLSLVKNLONIYFLYEGDPVTHENKSVQDLRSHDLIYVNSGPNYDKLT 90
QY 62 ELKNOEMATLFDKNDIDIVGEVYHLCYCENASERSACI-GGVNREGNHLLEIPKRIYVK 120
DB 91 ELKNOEMATLFDKNDIDIVGEVYHLCYCENASERSACI-GGVNREGNHLLEIPKRIYVK 150
QY 121 VSIDGIQSLSFDIETNKKMVTAEQELDYKRYKYLTDNKQLYTGSPSYETGYIKFIIPKNE 180
DB 151 VSIDGIQSLSFDIETNKKMVTAEQELDYKRYKYLTDNKQLYTGSPSYETGYIKFIIPKNE 210
QY 181 SFWFDFPEPEPTQSKYLMIVKDNFTLDSNT-QIEVYLYTK 220
DB 211 SFWFDFPEPEPTQSKYLMIVKDNFTLDSNTQIEVYLYTK 251

Search completed: June 23, 2003, 16:12:25
Job time : 69.3449 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 16:10:36 : Search time 12.9166 Seconds
(without alignments)
2102.722 Million cell updates/sec

Title: US-10-002-784A-16
Perfect score: 1322
Sequence: 1 MENKKVKLKKMFEVLYTLF.....KDNFTLDSNTSQIEVLYITK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues
Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published.Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCRT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCRTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1322	100.0	251	1	US-08-882-431-16
2	1322	100.0	251	1	US-10-002-784A-16
3	1308	98.9	251	8	US-08-973-391A-13
4	1136	85.9	220	9	US-10-002-784A-26
5	1136	85.9	468	9	US-10-002-784A-27
6	1075.5	81.4	250	9	US-09-870-759-20
7	576.5	43.6	266	9	US-09-870-759-10
8	576	43.6	239	10	US-09-150-947B-12
9	575	43.5	266	9	US-10-151-336-8
10	567.5	42.9	266	9	US-10-002-784A-6
11	563	42.6	239	9	US-10-002-784A-10
12	558.5	42.2	266	9	US-10-002-784A-8
13	558	42.2	239	1	US-08-882-431-10
14	553	41.8	266	1	US-08-882-431-14
15	553	41.8	266	9	US-10-002-784A-14
16	549	41.5	266	1	US-08-882-431-6
17	548	41.0	265	1	US-09-870-759-12
18	542	41.0	265	1	US-08-882-431-8
19	424	32.1	79	9	US-10-002-784A-39

20	340	25.7	258	9	US-09-870-759-14	Sequence 14, Appl
21	311	23.5	257	1	US-09-870-759-8	Sequence 8, Appl
22	307	23.2	257	9	US-08-882-431-2	Sequence 2, Appl
23	307	23.2	257	1	US-10-002-784A-2	Sequence 4, Appl
24	291.5	22.0	233	9	US-09-900-766-4	Sequence 4, Appl
25	291.5	22.0	233	9	US-09-900-766-4	Sequence 4, Appl
26	291.5	22.0	233	9	US-10-283-838-7	Sequence 7, Appl
27	290.5	22.0	217	9	US-09-900-766-6	Sequence 6, Appl
28	289.5	21.9	233	9	US-09-900-766-7	Sequence 7, Appl
29	289.5	21.9	233	9	US-10-283-838-8	Sequence 8, Appl
30	289	21.9	248	9	US-09-870-759-16	Sequence 16, Appl
31	283.5	21.4	233	1	US-08-882-431-4	Sequence 4, Appl
32	281.5	21.3	203	9	US-09-900-766-5	Sequence 5, Appl
33	277.5	21.0	233	9	US-09-900-766-3	Sequence 3, Appl
34	263.5	19.9	233	9	US-09-900-766-2	Sequence 2, Appl
35	263.5	19.9	672	9	US-09-900-766-1	Sequence 1, Appl
36	213.5	16.1	89	9	US-10-002-784A-37	Sequence 37, Appl
37	213.5	16.1	89	9	US-10-002-784A-38	Sequence 38, Appl
38	209.5	15.8	89	9	US-10-002-784A-36	Sequence 36, Appl
39	182.5	13.8	89	9	US-10-002-784A-35	Sequence 35, Appl
40	151	11.4	82	9	US-10-002-784A-33	Sequence 33, Appl
41	120	9.1	82	9	US-10-002-784A-34	Sequence 34, Appl
42	117.5	8.9	233	1	US-08-882-431-12	Sequence 12, Appl
43	116	8.8	234	9	US-10-002-784A-12	Sequence 12, Appl
44	115	8.7	82	9	US-10-002-784A-32	Sequence 32, Appl
45	109	8.2	234	9	US-09-870-759-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-882-431-16
; Sequence 16, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MAMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown

TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-16

Query Match 100.0%; Score 1322; DB 1; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.5e-110;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENKKVLLKKNVFFVLTFTGLTISOEVFAQODDPDSQLRSSLVKNLQNIYFLYEGDPV 60
DB 1 MENKKVLLKKNVFFVLTFTGLTISOEVFAQODDPDSQLRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKNOEMATLFFKKNVDIYGEVYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKNOEMATLFFKKNVDIYGEVYHLCYLC 120
QY 121 ENAERSACIYGVTNHEGNNLEIPKTIYKVSIDIGISLSPDIETNNKMTAQELDYKVR 180
DB 121 ENAERSACIYGVTNHEGNNLEIPKTIYKVSIDIGISLSPDIETNNKMTAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWMDFPEPEFTOSKYLIMYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWMDFPEPEFTOSKYLIMYKDNETLDSN 240
QY 241 TSOIEVYLTTK 251
DB 241 TSOIEVYLTTK 251

RESULT 2

US-10-002-784A-16

Sequence 16, Application US/10002784A
Publication No. US2003036644A1

GENERAL INFORMATION:

APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 16
LENGTH: 251
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
US-10-002-784A-16

Query Match 100.0%; Score 1322; DB 9; Length 251;
Best Local Similarity 100.0%; Pred. No. 9.5e-110;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENKKVLLKKNVFFVLTFTGLTISOEVFAQODDPDSQLRSSLVKNLQNIYFLYEGDPV 60
DB 1 MENKKVLLKKNVFFVLTFTGLTISOEVFAQODDPDSQLRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKNOEMATLFFKKNVDIYGEVYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKNOEMATLFFKKNVDIYGEVYHLCYLC 120
QY 121 ENAERSACIYGVTNHEGNNLEIPKTIYKVSIDIGISLSPDIETNNKMTAQELDYKVR 180
DB 121 ENAERSACIYGVTNHEGNNLEIPKTIYKVSIDIGISLSPDIETNNKMTAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWMDFPEPEFTOSKYLIMYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWMDFPEPEFTOSKYLIMYKDNETLDSN 240
QY 241 TSOIEVYLTTK 251

DB 241 TSOIEVYLTTK 251

RESULT 3

US-08-973-391A-13

Sequence 13, Application US/08973391A

Patent No. US20020054887A1

GENERAL INFORMATION:

APPLICANT: Schliervert, Patrick M.
APPLICANT: Roggliant, Manuela
APPLICANT: Stoehr, Jennifer
APPLICANT: Ohlendorf, Douglas
TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
FILE REFERENCE: 600,311USMO
CURRENT APPLICATION NUMBER: US/08/973,391A
CURRENT FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: PCT/US96/10252
PRIOR FILING DATE: 1996-06-07
PRIOR APPLICATION NUMBER: US 08/480,261
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent version 3.1
SEQ ID NO 13
LENGTH: 251
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-08-973-391A-13

Query Match 98.9%; Score 1308; DB 8; Length 251;
Best Local Similarity 99.2%; Pred. No. 1.7e-108;
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MENKKVLLKKNVFFVLTFTGLTISOEVFAQODDPDSQLRSSLVKNLQNIYFLYEGDPV 60
DB 1 MENKKVLLKKNVFFVLTFTGLTISOEVFAQODDPDSQLRSSLVKNLQNIYFLYEGDPV 60
QY 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKNOEMATLFFKKNVDIYGEVYHLCYLC 120
DB 61 THENVKSVDQLRSHDLIYNVSGPNYDKLTTELKNOEMATLFFKKNVDIYGEVYHLCYLC 120
QY 121 ENAERSACIYGVTNHEGNNLEIPKTIYKVSIDIGISLSPDIETNNKMTAQELDYKVR 180
DB 121 ENAERSACIYGVTNHEGNNLEIPKTIYKVSIDIGISLSPDIETNNKMTAQELDYKVR 180
QY 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWMDFPEPEFTOSKYLIMYKDNETLDSN 240
DB 181 KYLTDNKQLYTNGPSKYETGYIKFIPKNKESFWMDFPEPEFTOSKYLIMYKDNETLDSN 240
QY 241 TSOIEVYLTTK 251
DB 241 TSOIEVYLTTK 251

RESULT 4

US-10-002-784A-26

Sequence 26, Application US/10002784A

Publication No. US2003036644A1

GENERAL INFORMATION:

APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 26
LENGTH: 220
TYPE: PRT
ORGANISM: Artificial sequence

```

; FEATURE:
; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-A
US-10-002-784a-26

Query Match
Best Local Similarity 85.9%; Score 1136; DB 9; Length 220;
Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY 31 QODPPSOLHRSSLYVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 90
DB 2 QODPPSOLHRSSLYVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
QY 91 ELKNQEMATLTKKNDIYGEVYHLCYLCENARSACTGGVTNREGNHLTPKRIYVK 150
DB 62 ELKNQEMATLTKKNDIYGEVYHLCYLCENARSACTGGVTNREGNHLTPKRIYVK 120
QY 151 VSIDGIQSLSPDIETNKKMVAQELDYKVRKYLTDNKQLYTNGPSKYEYIKFIPKKE 210
DB 121 VSIDGIQSLSPDIETNKKMVAQELDYKVRKYLTDNKQLYTNGPSKYEYIKFIPKKE 180
QY 211 SFWDFPPEPFTQSKYLMYKDNELTDSNTSQIEVYLTTK 251
DB 181 SFWDFPPEPFTQSKYLMYKDNELTDSNT-QIEVYLTTK 220

RESULT 5
US-10-002-784a-27
; Sequence 27, Application US/10002784a
; Publication No. US2003003644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002.784a
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 27
; LENGTH: 468
; TYPE: PRF
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant Spea-mutant Speb fusion
US-10-002-784a-27

Query Match
Best Local Similarity 98.2%; Pred. No. 7.3e-93;
Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

QY 31 QODPPSOLHRSSLYVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 90
DB 2 QODPPSOLHRSSLYVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLKT 61
QY 91 ELKNQEMATLTKKNDIYGEVYHLCYLCENARSACTGGVTNREGNHLTPKRIYVK 150
DB 62 ELKNQEMATLTKKNDIYGEVYHLCYLCENARSACTGGVTNREGNHLTPKRIYVK 120
QY 151 VSIDGIQSLSPDIETNKKMVAQELDYKVRKYLTDNKQLYTNGPSKYEYIKFIPKKE 210
DB 121 VSIDGIQSLSPDIETNKKMVAQELDYKVRKYLTDNKQLYTNGPSKYEYIKFIPKKE 180
QY 211 SFWDFPPEPFTQSKYLMYKDNELTDSNTSQIEVYLTTK 251
DB 181 SFWDFPPEPFTQSKYLMYKDNELTDSNT-QIEVYLTTK 220

RESULT 6
US-09-870-759-20
; Sequence 20, Application US/09870759
; Patent No. US20020177551A1

; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRF
; ORGANISM: Streptococcus pyogenes
US-09-870-759-20

Query Match
Best Local Similarity 81.4%; Score 1075.5; DB 9; Length 250;
Matches 210; Conservative 7; Mismatches 33; Indels 1; Gaps 1;

QY 1 MENNKVYLKKMFVLYTLGLTISQEVFAQODPPSOLHRSSLYVKNLQNIYFLYEGDPV 60
DB 1 MENNKVYLKKMFVLYTLGLTISQEVFAQODPPSOLHRSSLYVKNLQNIYFLYEGDPV 60
QY 61 THENKSVQDLRSHDLIYNVSGPNYDKLKTTELKNQEMATLTKKNDIYGEVYHLCYLC 120
DB 61 THENKSVQDLRSHDLIYNVSGPNYDKLKTTELKNQEMATLTKKNDIYGEVYHLCYLC 120
QY 121 ENARSACTGGVTNREGNHLTPKRIYKVSIDGIQSLSPDIETNKKMVAQELDYKVR 180
DB 121 ENARSACTGGVTNREGNHLTPKRIYKVSIDGIQSLSPDIETNKKMVAQELDYKVR 179
QY 181 KYTLDNKQLYTNGPSKYEYIKFIPKKESEFWDFPPEPFTQSKYLMYKDNELTDSN 240
DB 180 KYTLDNKQLYTNGPSKYEYIKFIPKKESEFWDFPPEPFTQSKYLMYKDNELTDSN 239
QY 241 TSOIEVYLTTK 251
DB 240 TSOIEVYLTTK 250

RESULT 7
US-09-870-759-10
; Sequence 10, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-09-870-759-10

Query Match
Best Local Similarity 43.6%; Score 576.5; DB 9; Length 266;
Matches 123; Conservative 38; Mismatches 75; Indels 19; Gaps 7;

QY 15 VLVTFGLTIS-QEVFA-QODPPSOLHRSSLYVKNLQNIYFLYEGDPVTHENVKSVQ 70
DB 11 ILIFALIVISTPNTVAESQDPDELKRSKFTGLMKNKVALYDNNHVASAINVSIQ 70
QY 71 LRSHDLIYNVSGP---NYDKLTKTELKNQEMATLTKKNDIYGEVYHLCYLCEN----- 123
DB 71 FLVFDLIYSIKDKTKLGNIDNVKVEFKKDLADKTKDKYVYVPGANTYYQCFPSKTNNDIN 130
```

RESULT 9
 US-10-151-336-8
 Sequence 8, Application US/10151336
 Publication No. US20030079248A1
 GENERAL INFORMATION:
 APPLICANT: Mason, Hugh
 APPLICANT: Palmer, Kenneth
 APPLICANT: Hefteron, Kathleen
 APPLICANT: Mor, Tsafrit
 APPLICANT: Arentzen, Charles
 TITLE OF INVENTION: Geminal Virus Vectors for Gene Expression in Plants
 FILE REFERENCE: 4868/84453
 CURRENT APPLICATION NUMBER: US/10/151,336
 CURRENT FILING DATE: 2002-05-20
 PRIOR APPLICATION NUMBER: US/09/414,276

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RESULT 10-
US-10-002-784A-6
? Sequence 6, Application US/10002784A
? Publication No. US20030036644A1
? GENERAL INFORMATION:
?/33
? APPLICANT: Ulrich, Robert G.
? TITLE OF INVENTION: Bacterial Superantigen Vaccines
? FILE REFERENCE: 003/233/SAP
? CURRENT APPLICATION NUMBER: US/10/002,784A
? CURRENT FILING DATE: 2001-11-26
? PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
? PRIOR FILING DATE: 97-06-25; 98-09-01
? NUMBER OF SEQ ID NOS: 40
? SOFTWARE: Apple Macintosh Microsoft Word 6.0
? SEQ ID NO 6
? LENGTH: 266
? TYPE: prt
? ORGANISM: Artificial sequence
? FEATURE:
? OTHER INFORMATION: mutant staphylococcal enterotoxin B
US-10-002-784A-6

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[illegible]

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[illegible]

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11 MFV-FVLVTLGLTISCEVFAQDDPSQLHRSSLVKWL-ONITFLYEGDPVTHENVKSV 68
07
US-08-882-431-14 RESULT 14
; Sequence 14, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bayerl
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: John Moran
; STREET: US Army MRC-504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DERRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431-14
;
; Query Match 41.8%; Score 553; DB 1; Length 266;
; Best Local Similarity 44.9%; Pred. No. 2,2e-41;
; Matches 115; Conservative 51; Mismatches 72; Indels 18; Gaps 8;

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Db 12 LIFALLIJEFTPRVLA---SQPDPTPEBLKAKSFPTGLMENKVLLDDHIVSATKRV 68

Qy 69 DQLRSHDLIYNSG---PBYDKLTKELANOEATLEFKKANDIYGVETIYHLYC--ENA 123

Db 69 DKFRADHLLIYNSDKKLANIDKVKTELLNEGLAKYKDEVDVIGSNIVYFSSKDNV 128

Qy 124 ER---SACIYGGVYNHEGNNLEIP-KRIYKVSIDIGLSFDIEFTKNMWTAOELDY 177

Db 129 GKVTGKRTCMYGGITHEGNNHFDNGLNVLRIYVENKRNRISEEVYTDKSVYAOELDI 188

Qy 178 KVRKYLYTDKMLATDTPNGSPKRYETGYIKETIPKMKSEFDFPEP--EFTQSKYLYMIYKNE 235

Db 189 KARNFLINKNNIYEENFSYETGYIKETIENNNGNTWYDMAPGDKFDQSKYLYMAYDNK 248

Qy 236 TLDSNTSQTEVYLYITK 251

Db 249 IVDSKSKYRIEVLHLLTK 264

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RESULT 15
US-10-002-784A-14
Sequence 14, Application US/10002784A
Publication No. US2003005664A1
GENERAL INFORMATION:
/33
APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/9862,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 14
LENGTH: 266
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: staphylococcal enterotoxin C-1 mutant
US-10-002-784A-14

```

[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 16:10:06 ; Search time 18.5021 seconds
(without alignments)
1304.163 Million cell updates/sec

Title: US-10-002-784A-16

Perfect score: 1322

Sequence: 1 MNNKKVLKKNVFFVLVTFL.....KDNELTDSNTSQIEVYLTFTK 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1315	99.5	251	1	S29659
2	1239	93.7	236	2	S18783
3	1234	93.3	236	2	S18786
4	1109	83.9	236	2	S18789
5	1075.5	81.4	250	1	A26152
6	576.5	43.6	266	1	ENGAB6
7	551.5	41.7	266	2	S11885
8	549	41.5	266	2	A60114
9	548	41.5	266	1	ENSAC1
10	481	36.4	258	2	G89968
11	340	22.7	258	2	A31953
12	338	22.6	260	2	E89969
13	337	22.5	136	2	A89964
14	336	22.4	260	2	C89984
15	311.5	23.6	258	2	H89968
16	308	23.3	257	2	A28179
17	307	23.2	257	2	A28664
18	305.5	22.1	240	2	G89991
19	264	20.0	239	2	D89969
20	251.5	19.0	242	2	C89969
21	211	16.0	235	2	A30509
22	174	13.2	133	2	B89969
23	129.5	9.8	123	2	D89807
24	128	9.7	157	2	A89942
25	125	9.5	227	2	C89808
26	114	8.6	232	2	F89807
27	114	8.6	234	2	C89807
28	111	8.4	234	2	B89992
29	111	8.4	292	2	B89807

30	109.5	8.3	825	2	H82885	hypothetical prote
31	109	8.2	234	1	XCAS1	toxic shock syndr
32	108.5	8.2	231	2	H89806	exotoxin 7 (import
33	108.5	8.2	596	2	E96935	FUSON, methionine
34	108	8.2	436	2	T28342	ORF MSY181 hypote
35	108	8.2	493	2	G90604	hypothetical prote
36	105.5	8.0	1790	2	S67593	transport protein
37	105	7.9	770	2	B48910	desmocollin 1b pre
38	105	7.9	824	2	A48910	desmocollin 1a pre
39	105	7.9	840	2	I37281	Dscia precursor -
40	105	7.9	894	2	I37282	Dscib precursor -
41	104.5	7.9	1367	2	T18466	hypothetical prote
42	104.5	7.9	1856	2	C95008	immunoglobulin A1
43	103.5	7.8	241	2	B89888	hypothetical prote
44	103.5	7.8	396	2	S09627	prtc protein - Esc
45	103	7.8	235	2	C97252	probable membrane

ALIGNMENTS

Result 1
S29659
exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12
M:Alteinate names: erythrogenic toxin; scarlet fever toxin
C:Species: Streptococcus pyogenes phage T12
C:Date: 10-Sep-1999 #sequence.revision 10-Sep-1999 #text.change 10-Sep-1999
C:Accession: S29659, S18782, S18784, S18785, S18791, S18796, S18797, S18800
R:Weeks, C.R.; Ferretti, J.J.
Infect. Immun. 52, 144-150, 1986
A:Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin
A:Reference number: S29659; MUID:86166804; PMID:3514452
A:Accession: S29659
A:Molecule type: DNA
A:Residues: 1-251 <NEE>
A:Cross-References: GB:U04053; EMBL:M19350; NID:91877426; PIDN:MAC48868.1; PID:918774
A:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene en
A:Reference number: S18782; MUID:92044233; PMID:1940804
A:Accession: S18782
A:Status: nucleic acid sequence not shown; translation not shown
A:Residues: 1-251 <NEE>
A:Molecule type: DNA
A:Cross-References: EMBL:X61560; NID:947287; PIDN:CAA43758.1; PID:947288
A:Experimental source: Streptococcus pyogenes strain MGA5156 isolate Nebraska unassign
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18784
A:Status: nucleic acid sequence not shown; translation not shown
A:Residues: 1-251 <NEE>
A:Molecule type: DNA
A:Cross-References: EMBL:X61556; NID:947291; PIDN:CAA43754.1; PID:947292
A:Experimental source: Streptococcus pyogenes strain MGA5156 isolate Minnesota unassign
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18791
A:Status: nucleic acid sequence not shown; translation not shown
A:Residues: 1-251 <NEE>
A:Molecule type: DNA
A:Cross-References: EMBL:X61559; NID:947293; PIDN:CAA43757.1; PID:947294
A:Experimental source: Streptococcus pyogenes strain MGA5157 isolate Texas unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18796
A:Status: nucleic acid sequence not shown; translation not shown
A:Residues: 1-251 <NEE>
A:Molecule type: DNA
A:Cross-References: EMBL:X61555; NID:947309; PIDN:CAA43753.1; PID:947310
A:Experimental source: Streptococcus pyogenes strain MGA5157 isolate Arizona unassign
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18796
A:Status: nucleic acid sequence not shown; translation not shown
A:Residues: 1-251 <NEE>
A:Molecule type: DNA
A:Cross-References: EMBL:X61557; NID:947319; PIDN:CAA43755.1; PID:947320

A:Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18797
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NEB>
A:Cross-references: EMBL:X61558; NID:947321; PIDN:CAA43756.1; PID:947322
A:Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18800
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-228 <NEB>
A:Cross-references: EMBL:X61554; NID:947327; PIDN:CAA43752.1; PID:947328
A:Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: speA1
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1.30/Domain: signal sequence #status predicted <SIG>
F:31-251/Product: exotoxin type A #status predicted <MAT>

Query Match 99.5%; Score 1315; DB 1; Length 251;
Best Local Similarity .99.6%; Pred. No. 1.2e-90;
Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MENKKYKMKVFFVLTFLGTLTQSEVFAQODDPPSOLHRSLSLVKNQNTFLYEGDPV 60
DB 1 MENKKYKMKVFFVLTFLGTLTQSEVFAQODDPPSOLHRSLSLVKNQNTFLYEGDPV 60
OY 61 THENKSVDDLRSIDLTYNVSGBPNDKLTTELKQENATLFDKQNDIYGEVYHLCYL 120
DB 61 THENKSVDDLRSIDLTYNVSGBPNDKLTTELKQENATLFDKQNDIYGEVYHLCYL 120
OY 121 EMNERSACITGGVYTHNEGNHLEIPKTIYKVSIDGIOSLSFDIETNKKMTAQLDYKVR 180
DB 121 EMNERSACITGGVYTHNEGNHLEIPKTIYKVSIDGIOSLSFDIETNKKMTAQLDYKVR 180
OY 181 KYLDNMQLTNGSKETGYIKFIPKNKESFMDFPEPEPTOSKILMIYKDEETLDSN 240
DB 181 KYLDNMQLTNGSKETGYIKFIPKNKESFMDFPEPEPTOSKILMIYKDEETLDSN 240
OY 241 TSOIEVYLTTR 251
DB 241 TSOIEVYLTTR 251

RESULT 2

S18783
exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 iso1
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes phage
A:Variety: strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MG
C:Date: 29-Jan-1993 #sequence, revision 29-Jan-1993 #text, change 16-Jul-1999
A:Accession: S18783; S18793; S18794; S18801; S18798
J: Nelson, K.; Schlievert, P.M.; Seldander, R.K.; Musser, J.M.
C:Date: 29-Jan-1993 #sequence, revision 29-Jan-1993 #text, change 16-Jul-1999
A:Accession: S18782; MUID:92044323; PMID:1940804
A:Title: Characterization and clonal distribution of four alleles of the speA gene encod
A:Reference number: S18782; MUID:92044323; PMID:1940804
A:Accession: S18783
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEB>
A:Cross-references: EMBL:X61568; NID:947289; PIDN:CAA43766.1; PID:947290
A:Experimental source: strain MGAS158 isolate Nebraska unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18783
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEB>
A:Cross-references: EMBL:X61569; NID:947313; PIDN:CAA43767.1; PID:947314
A:Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18794
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEB>
A:Cross-references: EMBL:X61570; NID:947315; PIDN:CAA43768.1; PID:947316
A:Experimental source: strain MGAS491 isolate United Kingdom unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18801
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEB>
A:Cross-references: EMBL:X61572; NID:947333; PIDN:CAA43770.1; PID:947334
A:Experimental source: strain MGAS624 isolate Germany unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18798
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEB>
A:Cross-references: EMBL:X61571; NID:947323; PIDN:CAA43769.1; PID:947324
A:Experimental source: strain MGAS495 isolate Germany unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
C:Genetics:
A:Gene: speA3
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1.32/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 93.7%; Score 1239; DB 2; Length 236;
Best Local Similarity 99.2%; Pred. No. 4.8e-85;
Matches 234; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 9 KKMFFVLYVFLGTLTQSEVFAQODDPPSOLHRSLSLVKNQNTFLYEGDPVTHENKSV 68
DB 1 KKMFFVLYVFLGTLTQSEVFAQODDPPSOLHRSLSLVKNQNTFLYEGDPVTHENKSV 68
OY 69 DQLRSHDLIYVNSGPNDKLTTELKQENATLFDKQNDIYGEVYHLCYCEAERSAC 128
DB 69 DQLRSHDLIYVNSGPNDKLTTELKQENATLFDKQNDIYGEVYHLCYCEAERSAC 128
OY 129 IYGGVTHNEGNHLEIPKTIYKVSIDGIOSLSFDIETNKKMTAQLDYKVRKYLTDNKQ 188
DB 129 IYGGVTHNEGNHLEIPKTIYKVSIDGIOSLSFDIETNKKMTAQLDYKVRKYLTDNKQ 188
OY 189 LYTNGPSKYEYGYIKFIPKNKESFMDFPEPEPTOSKILMIYKDEETLDSNISOI 244
DB 189 LYTNGPSKYEYGYIKFIPKNKESFMDFPEPEPTOSKILMIYKDEETLDSNISOI 244
OY 244 TSOIEVYLTTR 251
DB 244 TSOIEVYLTTR 251

RESULT 3

S18786
exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 1
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes phage
A:Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; stra
C:Date: 29-Jan-1993 #sequence, revision 29-Jan-1993 #text, change 16-Jul-1999
A:Accession: S18786; S18787; S18788; S18790; S18792; S18795; S18799
J: Nelson, K.; Schlievert, P.M.; Seldander, R.K.; Musser, J.M.
C:Date: 29-Jan-1993 #sequence, revision 29-Jan-1993 #text, change 16-Jul-1999
A:Accession: S18786
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEB>
A:Cross-references: EMBL:X61561; NID:947297; PIDN:CAA43759.1; PID:947298
A:Experimental source: strain MGAS250 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
A:Accession: S18787
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

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A:Residues: 1-236 <NE>
A:Cross-references: EMBL.X61562; NID:g47299; PIDN:CAA43760.1; PID:g47300
A:Experimental source: strain MGAS251 isolate California unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18788
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL.X61563; NID:g47301; PIDN:CAA43761.1; PID:g47302
A:Experimental source: strain MGAS256 isolate California unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18790
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL.X61564; NID:g47305; PIDN:CAA43762.1; PID:g47306
A:Experimental source: strain MGAS285 isolate Colorado unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18792
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL.X61565; NID:g47311; PIDN:CAA43763.1; PID:g47312
A:Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18795
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL.X61566; NID:g47317; PIDN:CAA43764.1; PID:g47318
A:Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18799
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NE>
A:Cross-references: EMBL.X61567; NID:g47325; PIDN:CAA43765.1; PID:g47326
A:Experimental source: strain MGAS496 isolate Germany unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: speA2
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <Sig>
F:23-236/Product: exotoxin type A (fragment) #status predicted <Ant>

Query Match          93.3%; Score 1234; DB 2; Length 236;
Best Local Similarity 99.2%; Pred. No. 1.le-84;
Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      9 KKMVFVLYVTFLGLTISEVFAOODPPPSOLHRSSLVKNLONITYFLTEGDPVTHENKSV 68
        |||
Db       1 KKMFFVLVLTFLGLTISOEVAQODPPDSOLHRSSLVKNLONITFLTEGDVTHENKSV 60

OY      69 DQLRSHDLIYNVSGPNTDKLTELNQEMATLFKDNVDIYGEVYHLICYLECAEAERSAC 128
        |||
Db       61 DQLLSHDLIYNVSGPNTDKLTELNQEMATLFDKNVDIYSEVYHLICYLECAEAERSAC 120

OY      129 IYGGVTHHEGHLEIPRKIVYKSIDIGIOSLSPDIEFNKKKWTAQOEILDYKRYKTLTDNKQ 188
        |||
Db       121 IYGGVTHHEGHLEIPRKIVYKSIDIGIOSLSPDIEFNKKKWTAQOEILDYKRYKTLTDNKQ 180

OY      189 LYTNGPSKYENGKFTPKNKESFWDFEPPEPTQSXYLMAYDNETLDSNTSQT 244
        |||
Db       181 LYTNGPSKYENGKFTPKNKESFWDFEPPEPTQSXYLMAYDNETLDSNTSQI 236

RESULT 4
S18789
exotoxin A precursor (alllele 4) - Streptococcus pyogenes (strain MGAS262 isolate Califor
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes
V:Variety: strain MGAS262 isolate California
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C.Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C.Accession: S18789
R.Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A.Title: Characterization and clonal distribution of four alleles of the speA gene
A.Reference number: S18782; MUID:92044323; PMID:1940804
A.Accession: S18789
A>Status: nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-236 <NEW>
A.Cross-references: EMBL:X61573; NID:q47303; PIDN:CAA43771.1; PID:q47304
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1999
C.Genetics:
A.Gene: speA
C.Superfamily: enterotoxin B
C.Keywords: exotoxin
F.1-22/Domain: signal sequence (fragment) #status predicted <Sig>
F.23-236/Product: exotoxin A (fragment) #status predicted <Mat>

Query Match      83.9%  Score 1109; DB 2; Length 236;
Best Local Similarity 88.6%  Pred. No. 2.3e-73;
Matches 209; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

OY 9 KMAVFVATFTEGLITISOEFAQQDDPSQSHRSSLVNKNITFLYEGDPVTHENVKSV 68
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 KRIYFVLAIIFGLTTSQSEFAQQDPNPSQSHRSSLVNKNITFLYEGDPVTHENVKSV 60
OY 69 DQLRSHDLIYVNSGNYDKRLTELKNQEMATLFFDKNVDIYGEVYHLCYCENAESAC 128
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 DQLSHDLIYVNSGNYDKRLTELKNREMSLFFRNKNVDIYGEVYHLCYCRNAKRAC 120
OY 129 IYGVYTNHEGNHLEIPKKIIVKSIDGQSLSFDLETNKKVYTAQOELDYKRYKLTPTNKO 188
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 IYGVYTNHEGNHLEIPKKIIVKSIDGQSLSFDLETNKKVYTAQOELDYKRYKLTPTNKO 180
OY 189 LYTNGPSKYETGYIKFIDPKNKESEFWDFEPPEFTQSKYIMTYKDNFTLDSNTSQI 244
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 181 LYTNGPSKYETGYIKFIDPKNKESEFWDFEPPEFTQSKYIMTYKDNFTLDSNTSQI 236

RESULT 5
A26152
Streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
N.Alternate names: scarlet fever toxin; SPE type A (speA)
C.Species: Streptococcus sp.
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: A26152
R.Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A.Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to
A.Reference number: A26152; MUID:86284313; PMID:3526093
A.Molecule type: DNA
A.Residues: 1-250 <JOH>
C.Superfamily: enterotoxin B
C.Keywords: exotoxin

Query Match      81.4%  Score 1075.5; DB 1; Length 250;
Best Local Similarity 83.7%  Pred. No. 7.5e-73;
Matches 210; Conservative 7; Mismatches 33; Indels 1; Gaps 1;

OY 1 MNNKKVLLKKWVFVLTFLGLTTSQEVFAQQDDPSQSHRSSLVNKNITFLYEGDPV 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 MNNKEVLLKKWVFVLMKFLGLTTLIPKQICSTPRKPSQSLNSLTKFKIYIFPMRYTLV 60
OY 61 THENKVSVDQLRSHDLIYVNSGPNYDKRLTELKNQEMATLFFDKNVDIYGEVYHLCYLC 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 THENKVSVDQLRSHDLIYVNSGPNYDKRLTELKNQEMATLFFDKNVDIYGEVYHLCYLC 120
OY 121 ENAESACIYGVYTNHEGNHLEIPKKIIVKSIDGQSLSFDLETNKNKMYTAQOELDYKVR 180
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 ENAESACIYGVYTNHEGNHLEIPKKIIVKSIDGQSLSFDLETNKNKMYTAQOELDYKVR 179

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Qy 181 KYLDNKKOLYNGPSKYEYIKFIPKNESEFDFEPFEPFOSKYLMIYKDNETLDSN 240
 Db 180 KYLDNKKOLYNGPSKYEYIKFIPKNESEFDFEPFEPFOSKYLMIYKDNETLDSN 239
 Qy 241 TSOIEVYLTTR 251
 Db 240 TSOIEVYLTTR 250

RESULT 6

ENSAB6

enterotoxin B precursor - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 24-Apr-1984 #sequence, revision 15-Oct-1996 #text_change 18-Jun-1999

C:Accession: S27360; A92065; S27240; A01815

R:Jones, C.L.; Khan, S.A.

J. Bacteriol. 166, 29-33, 1986

A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.

A:Reference number: S27360; MUID:86168029; PMID:3957869

A:Accession: S27360

A:Molecule type: DNA

A:Residues: 1-266 <ON>

A:Cross-references: EMBL:M11118; NID:9152999; PIDN:AAA88550.1; PID:9153000

A:Experimental source: strain S6

R:Huang, I.Y.; Bergdoll, M.S.

J. Biol. Chem. 245, 3518-3525, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide

A:Reference number: A92065; MUID:71007902; PMID:5470821

A:Accession: A92065

A:Molecule type: protein

A:Residues: 28-55, 'NMD', '59-68', 'NE', '71', 'FDLIVL', '78-117', '119-127', 'N', '129', 'D', '131-132', 'ENT',

A:Experimental source: strain S-6

R:Huang, I.Y.; Bergdoll, M.S.

J. Biol. Chem. 245, 3511-3517, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, composition

A:Reference number: A92064; MUID:71007901; PMID:5470820

A:Contents: annotation; chymotryptic peptides

R:Huang, I.Y.; Bergdoll, M.S.

J. Biol. Chem. 245, 3493-3510, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composition

A:Reference number: A92063; MUID:71007900; PMID:5470819

A:Contents: annotation; tryptic peptides

R:Schantz, E.J.; Roessler, W.G.; Wagnan, J.; Spero, L.; Dunnehy, D.A.; Bergdoll, M.S.

Biochemistry 4, 1011-1016, 1965

A:Title: Purification of staphylococcal enterotoxin B.

A:Reference number: A90548; MUID:66035792; PMID:4953912

A:Contents: annotation, biological source of protein

R:Alakhov, V.I.; Kilmory, E.Y.; Kolesov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshni

Eur. J. Biochem. 209, 823-828, 1992

A:Title: Identification of functionally active fragments of staphylococcal enterotoxin B

A:Reference number: S27240; MUID:93049338; PMID:1425690

A:Accession: S27240

A:Molecule type: protein

A:Residues: 28-42, 128-148 <ALA>

C:Superfamily: enterotoxin B

C:Keywords: enterotoxin; extracellular protein; toxin

F:1-27/Domain: signal sequence predicted <SIG>

F:28-266/Product: enterotoxin B #status experimental <MAT>

F:120-140/Disulfide bonds: #status experimental

Query Match

Best Local Similarity 43.6%; Score 576.5; DB 1; Length 266;

Matches 123; Conservative 36; Mismatches 75; Indels 19; Gaps 7;

Qy 15 VLVTFLGLTIS-QEVFA--QDDPDSOLHSSSLVKNL-QNITFLYEDDPYTHENKVSVDQ 70

Db 11 ILFLFALLIVISTPNVLAESQDPDPDLHSSSKFTGMENMKKLYDDNHYSAINVKSIDQ 70

Qy 71 LRSHDLIYVNSGP---NYDKLKTETLKNOEMATLFKDRKNDIYGVYHLGYLCA-- 123

Db 71 FLKFDLITISKDKRLKNGIDNVRKFEKNDLADKKDYVYFGANNIYQCFSSKRTMDIN 130

Qy 124 ----ERSACIYGGVTNHEGNNHLEIPKKIYVKSIDGISOISFDIETNKKMVTAAQELDYK 178

Db 131 SHQDTRKKTOMGVTEHNGNQLDKYRSLIVRVEDCKNLISFDVQTNKKKVTAAQELDYK 190
 Qy 179 VKRITLDNKKOLYNGPSKYEYIKFIPKNESEFDFEPFEPFOSKYLMIYKDNET 236
 Db 191 TRHYLVNKKRLYEFNNSPYETGYIKFI-ENENSPWYDMPAPGDKFOSKYLMIYKDN 249
 Qy 237 LDSNTSOIEVYLTTR 251
 Db 250 VDSKOVKIEVYLTTR 264

RESULT 7

S11885

enterotoxin C3 - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 19-Mar-1997 #sequence, revision 19-Mar-1997 #text_change 16-Jul-1999

C:Accession: S11885

R:Howe, C.J.; Hackett, S.P.; Bohach, G.A.

Mol. Gen. Genet. 220, 329-333, 1990

A:Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comp

A:Reference number: S11885; MUID:90220508; PMID:2325627

A:Accession: S11885

A:Molecule type: DNA

A:Status: preliminary

A:Residues: 1-266 <BOH>

A:Cross-references: GB:X51661; NID:946570; PIDN:CAA35972.1; PID:946571

C:Superfamily: enterotoxin B

Query Match

Best Local Similarity 41.7%; Score 551.5; DB 2; Length 266;

Matches 117; Conservative 46; Mismatches 74; Indels 17; Gaps 8;

Qy 15 VLVTFLGLTIS-QEVFAQDDP--PSOLHSS-LVKNLQNIYFLYEDDPYTHENKVSVDQ 70

Db 11 ILFLFALLIVISTPNVLAESQDPDPDLHSSSEFTGTGMKKLYDDHYVSAIKVKSVDK 70

Qy 71 LRSHDLIYVNSGP---PNYDKLKTETLKNOEMATLFKDRKNDIYGVYHLGYLCA--ENAER 125

Db 71 FLAHDILYNSDKRLKRYDKVKTFLNEDLAKKKDEVDYGSNYYVNCYFSSKONVCK 130

Qy 126 ----SACIYGGVTNHEGNNHLEIP--KKIYVKSIDGISOISFDIETNKKMVTAAQELDYK 179

Db 131 VTGKRTOMGVITGHEGNNHFDGNGNLQNVLAIRVENKRNNTISFEVOTKKKSTAAQELDIKA 190

Qy 180 RKYITLDNKKOLYNGPSKYEYIKFIPKNESEFDFEPFEPFOSKYLMIYKDNETL 237

Db 191 RNFINKKNLYEFNNSPYETGYIKFIENNGTFWYDMPAPGDKFOSKYLMIYKDN 250

Qy 238 DSNTSOIEVYLTTR 251

Db 251 DSKSVKIEVYLTTR 264

RESULT 8

A60114

enterotoxin C-2 precursor - Staphylococcus aureus

N:Alternate names: enterotoxin C-3 precursor

C:Species: Staphylococcus aureus

C:Date: 10-Nov-1992 #sequence, revision 10-Nov-1992 #text_change 16-Jul-1999

C:Accession: A60114; B60114; A33866

R:Bohach, G.A.; Schlievert, P.M.

Infect. Immun. 57, 2249-2252, 1989

A:Title: Conservation of the biologically active portions of staphylococcal enterotox

A:Reference number: A60114; MUID:89277549; PMID:2543637

A:Accession: A60114

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-266 <BOH>

A:Molecule type: protein

A:Residues: 28-66 <BOH2>

R:Couch, J.L.; Betley, M.J.

R:Bayles, K.W.; Iandolo, J.J.
 J. Bacteriol. 171, 4799-4806, 1989
 A:Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin
 A:Reference number: A33953; MUID:89359112; PMID:2549000
 A:Accession: A33953
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-258 <BAV>
 A:Cross-references: GB:M28521; NID:q1492109; PIDN:BA06195.1; PID:g758691
 C:Superfamily: enterotoxin B

Query Match 25.78; Score 340; DB 2; Length 258;
 Best Local Similarity 35.28; Pred. No. 4e-18;
 Matches 92; Conservative 47; Mismatches 102; Indels 20; Gaps 10;

QY 8 LKKMVFVLTGLTISQ-EVFAODDP---PSQLR---SSLVKNLQNYFLYEG 57
 Db 1 MKFNITALLFTSLVSPLVNKNENIDSVKEKELHKKSELSSTALNNKHSY -ADK 58
 QY 58 DPVTHENVKSVQDLRSHDLIYN---VSGPNYDKLTKELKNOEMATLEKKNVDYGVERY 114
 Db 59 NPILGKSTGDFLENTLLYKFFFDLINFEDLINENSKEMAOHFKSNVDYPIRYS 118
 QY 115 HLCYGENMRSACITGVTNHEGNHLEIPKTIYKVSIDGIC-SLSPD-IETNKKMVT 172
 Db 119 INCYGE-IDRTACTYGVTPHEGNKLEKRIPIMLINGVQKEVSLDKVQTDKKNVTY 177
 QY 173 QELDYVRRYLTNDKQLYTNGP--SKETGYIKFIPKNKESFMPFEPETOSKYLM 230
 Db 178 QELDAQRRYLTNDKLYNNDTLGGKIQKIEFPSSDSKVSYLEDKGDFPEKQLRI 237
 QY 231 YNDNETLDSNTSQIEVYLT 251
 Db 238 YSDNKLSTELHLDIYLEK 258

RESULT 12
 E89969
 enterotoxin Seo [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: E89969
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: E89969
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-260 <KUR>
 A:Cross-references: GB:BA000018; PID:g13701623; PIDN:BA042916.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: seo
 C:Superfamily: enterotoxin B

Query Match 25.68; Score 338; DB 2; Length 260;
 Best Local Similarity 36.28; Pred. No. 5.6e-18;
 Matches 96; Conservative 42; Mismatches 107; Indels 20; Gaps 9;

QY 1 MKNKKVLLKMKVFPVLTGLTISQEVFA-QODPPPSQLHRSILK--NLQIYFLYEG 57
 Db 1 MKNKKVLLKMKVFPVLTGLTISQEVFA-QODPPPSQLHRSILK--NLQIYFLYEG 57
 QY 58 DPVTHENVKSV---DQLRSHDLIYN---VSG--PNYKLTTELKNOEMATLEKKNVD 107
 Db 59 NPILGKSTGDFLENTLLYKFFFDLINFEDLINENSKEMAOHFKSNVDYPIRYS 118
 QY 108 IYGVYTHLCLYENMRSACITGVTNHEGNHLEIPKTIYKVSIDGICSLSPDIEK 167
 Db 117 IYGVYTHLCLYENMRSACITGVTNHEGNHLEIPKTIYKVSIDGICSLSPDIEK 167

QY 168 KVAQOELDYKVRKYLTDNKLQLYTNGPSKYETGYIKF--IKKNESFWEDEFPEPTOS 225
 Db 176 KVAQOELDYKVRKYLTDNKLQLYTNGPSKYETGYIKF--IKKNESFWEDEFPEPTOS 225
 QY 226 KYLMYTKDNETLDSNTSQIEVYLT 250
 Db 236 QYLYQYNDKNTLDSNTSQIEVYLT 250

RESULT 13
 A89969
 enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: A89969
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: A89969
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-136 <KUR>
 A:Cross-references: GB:BA000018; PID:g13701619; PIDN:BA042912.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: yent2

Query Match 25.58; Score 337; DB 2; Length 136;
 Best Local Similarity 49.68; Pred. No. 2.9e-18;
 Matches 67; Conservative 22; Mismatches 38; Indels 8; Gaps 2;

QY 125 RSACIYGVYTHNEGNHLEIPKTIYKVSIDGICSLSPDIEKKNVTAQELDYK 178
 Db 2 KKTGMGVYTHNEGNHLEIPKTIYKVSIDGICSLSPDIEKKNVTAQELDYK 178
 QY 179 VRRYLTNDKQLYTNGPSKYETGYIKFIPKNKESFWEDEFPE--PEPTOSKYLMYKDN 236
 Db 62 VRRYLTNDKQLYTNGPSKYETGYIKFIPKNKESFWEDEFPE--PEPTOSKYLMYKDN 236
 QY 237 LDSNTSQIEVYLT 251
 Db 122 VESKSLNVEVYHLEK 136

RESULT 14
 C89984
 enterotoxin P [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: C89984
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: C89984
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-260 <KUR>
 A:Cross-references: GB:BA000018; PID:g13701743; PIDN:BA043036.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: sep
 C:Superfamily: enterotoxin B

Query Match 25.48; Score 336; DB 2; Length 260;
 Best Local Similarity 34.18; Pred. No. 7.9e-18;
 Matches 91; Conservative 52; Mismatches 86; Indels 38; Gaps 13;

```

RESULT 15
H89968
enterotoxin Sen [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: H89968.
R:Kurodo, M.; Ohte, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Oi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89968
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 (<RUR>)
A:Cross-references: GB:BA000018; PUD:g13701618; PIDN:BA042911.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: sen
C:Superfamily: enterotoxin B

```

QY	1	MENNKKYVKKKVVFF--VLVTFELGLTISOEVAOOD---PPPSOLHRSILVKNQNY- 52
Db	1	MKNIKKLMR--LFYIAAIIITLCLINNHYVAEDKDKKKKSDSDSKLF- NLTSYIT 57
QY	53	-FLYEGDPVTHENKYSVDOLRSHDL--YVNSGPYDILKLTELKNQEMATLEKKNVDI 108
Db	58	DITWOLD---ESMKISTDOLLNNTLITIKNIDISVLTSSLKLEFNSSDLANOFKKNIDI 114
QY	109	YGVVEYHHCY-LCEAERSACIYGVTHNEGHMLEPKRIYKVSIDGISOLSFDEJTNK 167
Db	115	YGLTFGNKCVGILTE--EKTSCILYGVTHIDGNOLOBEKYIGAVNEKDGVOOEGEVATKTK 172
QY	168	KAVTAQELDHYKVRKYLITDNKOLYTPGKPSKRYEYGIKFIPIKN--KESFWDFPEPEPFTOS 225
Db	173	AKVYVQELDGTVYRFLTENLKYIKYNDGTGIGKGCIFEFHSHNQDPSFYIDLYVKKSVGA 232
QY	226	KYLMATIKKNEITLSDTSTQIEVYL 248
Db	233	EFQFYSDNRKTVSSSNYHIDVFL 255

Search completed: June 23, 2003, 16:15:54
Job time : 20.5021 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 16:06:40 ; Search time 9.77469 Seconds

(without alignments)
1065.053 Million cell updates/sec

Title: US-10-002-784A-16

Perfect score: 1322

Sequence: 1 MKNKKVLLKKMVFVLYVTL.....KDNETLDNTSQIEVYLPTK 251

Scoring table: BIOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Swissprot_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1125	99.5	251	1	SP6A_STRPY
2	576.5	43.6	266	1	ETXB_STAUV
3	551.5	41.7	266	1	ETC3_STAUV
4	549	41.5	266	1	ETC2_STAUV
5	548	41.5	266	1	ETC1_STAUV
6	481	36.4	258	1	ETXG_STAUV
7	340	25.7	258	1	ETXD_STAUV
8	308	23.3	257	1	ETXE_STAUV
9	307	23.2	257	1	ETXA_STAUV
10	215	16.3	235	1	SPEC_STRPY
11	212.5	16.1	235	1	SP6H_STRPY
12	165	12.5	234	1	SP6G_STRPY
13	109	8.2	1790	1	TSTST_STAUV
14	105.5	8.0	1790	1	USOL_YEAST
15	105	7.9	894	1	DSCI_HUMAN
16	103.5	7.8	396	1	PRRC_ECOLI
17	98	7.4	908	1	DPOL_BORBU
18	95	7.2	427	1	V5SA_HSV7
19	94.5	7.1	807	1	HISA_STAUV
20	94.5	7.1	2151	1	RRLP_SEOUB
21	93.5	7.1	999	1	HGP2_HAEIN
22	93	7.0	405	1	TACY_CLOPE
23	92.5	7.0	405	1	DBR1_YEAST
24	91	6.9	303	1	VANY_ENTRC
25	90.5	6.8	893	1	DSCI_BOVIN
26	90	6.8	1956	1	ATX1_PLAFA
27	89.5	6.8	724	1	P85A_MOUSE
28	89.5	6.8	2410	1	POL1_BAYM
29	89	6.7	554	1	Y478_RICPR
30	88.5	6.7	357	1	SP11_RABPU
31	88.5	6.7	495	1	Y243_MOUSE
32	88.5	6.7	540	1	MTAL_ACICA
33	88.5	6.7	993	1	HGBC_HAEIN

ALIGNMENTS

RESULT 1	ID	SP6A_STRPY	STANDARD:	PRT:	251 AA.
AC	P08095:				
DT	01-AUG-1988 (rel. 08, Created)				
DT	01-JAN-1990 (rel. 13, Last sequence update)				
DT	15-JUN-2002 (rel. 41, Last annotation update)				
DE	Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin) (SPE A).				
GN	SP6A OR SP6M18.0393.				
OS	Streptococcus pyogenes, and				
OS	Streptococcus pyogenes (serotype M18).				
OC	Bacteria: Firmicutes; Lactobacillales; Streptococcaceae;				
OC	Streptococcus.				
OX	NCBI_TaxID=1314, 186103;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=86166804; PubMed=3514452;				
RA	Weeks C.R., Ferretti J.J.;				
RT	*Nucleotide sequence of the type A streptococcal exotoxin				
RT	(erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage				
RT	T12.*;				
RL	Infect. Immun. 52:144-150(1986).				
RL	[2]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=86284313; PubMed=3526093;				
RX	Johnson L.P., L'Italien J.J., Schlievert P.M.;				
RA	*Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is				
RT	related to Streptococcus aureus enterotoxin B.*;				
RT	Mol. Gen. Genet. 203:354-356(1986).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MGAS8232 / Serotype M18;				
RX	MEDLINE=21927593; PubMed=11917108;				
RA	Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,				
RA	Sylla G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,				
RA	Parfins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,				
RA	Kaput V., Daly J.A., Veasy L.G., Muser J.M.;				
RT	*Genome sequence and comparative microarray analysis of serotype M18				
RT	group A Streptococcus strains associated with acute rheumatic fever				
RT	outbreaks.*;				
RT	Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).				
RL	[4]				
RN	X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).				
RX	MEDLINE=99094887; PubMed=9878045;				
RA	Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,				
RA	O'Brien G.M., Tranter H.S., Acharya K.R.;				
RT	*Structural basis for the recognition of superantigen streptococcal				
RT	pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell				
RT	receptors.*;				
RL	EMBO J. 18:9-21(1999).				
CC	-1- SUBUNIT: Binds to major histocompatibility complex class II beta				
CC	chain.				
CC	-1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE				
CC	THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET				
CC	FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE				

CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
 CC FEVER.
 CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
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 CC -----
 DR EMBL: U04053; AAC48868.1; -
 DR EMBL: X03929; CAA27568.1; -
 DR EMBL: AE009982; AAL97141.1; -
 DR PIR: A26152; A26152.
 DR PIR: S29659; S29659.
 DR PDB: 1B1Z; 24-NOV-99.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_Strep_toxin; 1.
 DR Pfam: PF02876; Staph_Strep_toxin; 1.
 DR PRINTS: PR00279; BACTRUTOXIN.
 DR PROSITE: PS00227; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Toxin; Signal; 3D-structure.
 KW SIGNAL 1 30
 FT CHAIN 31 251 EXOTOXIN TYPE A.
 FT DISULFID 117 128
 FT CONFLICT 17 6 K -> E (IN REF. 2).
 FT CONFLICT 17 18 VT -> MK (IN REF. 2).
 FT CONFLICT 25 35 SOEYFAQDDP -> LFKGICSTRPK (IN REF. 2).
 FT CONFLICT 40 40 H -> Q (IN REF. 2).
 FT CONFLICT 43 43 S -> N (IN REF. 2).
 FT CONFLICT 47 59 NLQNIYFLYEGDP -> TFKIYIFEMAVTL (IN
 FT REF. 2).
 FT CONFLICT 129 129 I -> L (IN REF. 2).
 FT CONFLICT 165 178 TNKMYAQLDVR -> QIKNGCSRISYT (IN
 FT REF. 2).
 SQ SEQUENCE 251 AA; 29246 MW; 54001FE4CCBFC3 CRC64;
 Query Match 99.54; Score 1315; DB 1; Length 251;
 Best Local Similarity. 99.66; Pred. No. 8.6e-93;
 Matches 250; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MNNKKVKKKMFVLTFLGLTISQEVFAQDDPDSQLRRSLVKNLQNIYFLYEGDPV 60
 DB 1 MNNKKVKKKMFVLTFLGLTISQEVFAQDDPDSQLRRSLVKNLQNIYFLYEGDPV 60
 QY 61 THENVSVDDLRLSHDLIYNVSGPNYDKLTETLNQEMATLFKKNVDIYGEVYHLCYLC 120
 DB 61 THENVSVDDLRLSHDLIYNVSGPNYDKLTETLNQEMATLFKKNVDIYGEVYHLCYLC 120
 QY 121 ENMERASCIYGVNTNHEGNLEIPKTIYVAVSIDGIQSLSPDIETNKKMTAQLDYKVR 180
 DB 121 ENMERASCIYGVNTNHEGNLEIPKTIYVAVSIDGIQSLSPDIETNKKMTAQLDYKVR 180
 QY 181 KYLTDNKQLYTNQSPKYEYGIKFIPIPNKSEFWEDEFPPEPFOSKTLIMIKONETLDSN 240
 DB 181 KYLTDNKQLYTNQSPKYEYGIKFIPIPNKSEFWEDEFPPEPFOSKTLIMIKONETLDSN 240
 QY 241 TSQIEVYLTTR 251
 DB 241 TSQIEVYLTTR 251
 RESULT 2
 ETXB_STRAU STANDARD; PRT; 266 AA.
 AC P01552;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Enterotoxin type B precursor (SEB).
 GN ENTB.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66168029; Pubmed=3957869;
 RA Jones C.L., Khan S.A.;
 RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus
 RT aureus.";
 RL J. Bacteriol. 166:29-33(1986).
 RN [2]
 RP SEQUENCE OF 40-91 FROM N.A.
 RX MEDLINE=8529825; Pubmed=3898073;
 RA Ranelletti D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
 RT "Molecular cloning of staphylococcal enterotoxin B gene in
 RT Escherichia coli and Staphylococcus aureus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
 RN [3]
 RP SEQUENCE OF 28-266 (S-6).
 RX MEDLINE=71007902; Pubmed=5470821;
 RA Huang I.-Y., Bergdoll M.S.;
 RT "The primary structure of staphylococcal enterotoxin B. 3. The
 RT cyanogen bromide peptides of reduced and aminoethylated enterotoxin
 RT B, and the complete amino acid sequence.";
 RL J. Biol. Chem. 245:3518-3525(1970).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=93063291; Pubmed=1436058;
 RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
 RT "Crystal structure of staphylococcal enterotoxin B, a superantigen.";
 RL Nature 359:801-806(1992).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
 RX MEDLINE=94203282; Pubmed=8152483;
 RA Jaderczyk T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,
 RA Chl Y.I., Stauffer C., Strominger J.L., Wiley D.C.;
 RT "Three-dimensional structure of a human class II histocompatibility
 RT molecule complexed with superantigen.";
 RL Nature 368:711-718(1994).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
 RX MEDLINE=99096298; Pubmed=9881971;
 RA Li H., Ilerra A., Tsuchiya D., Leder L., Ysearn X., Schlievert P.M.,
 RA Karjalainen K., Mariuzza R.A.;
 RT "Three-dimensional structure of the complex between a T cell receptor
 RT beta chain and the superantigen staphylococcal enterotoxin B.";
 RL Immunity 9:807-816(1998).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RX MEDLINE=98181012; Pubmed=9514739;
 RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;
 RT "Crystal structure of microbial superantigen staphylococcal
 RT enterotoxin B at 1.5-A resolution: implications for superantigen
 RT recognition by MHC class II molecules and T-cell receptors.";
 RL J. Mol. Biol. 277:61-79(1998).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
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 EMBL: M1118; AAA88550.1; -

[illegible][illegible]

QY 180 RXYLDNKKOLYTNQPSKYETGYIKFIPKKESEFDFPEP--EFTQSKYLMYKDNETL 237
 DB 191 RNFINKKNLYENSSPYETGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMYKDNKTV 250
 QY 238 DSNTSOIEVYLTK 251
 DB 251 DSKSVKIEVHLTK 264

RESULT 4
 ETC2_STAU STANDARD; PRT: 266 AA.
 ID ETC2_STAU STANDARD; PRT: 266 AA.
 AC P34071;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Enterotoxin type C-2 precursor (SEC2).
 GN EMTC2.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_Taxid=1280;
 RN [1]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 28-66.
 RX MEDLINE=89277549; PubMed=2543637;
 RA Bohach G.A., Schlievert P.M.;
 RT "Conservation of the biologically active portions of staphylococcal
 RT enterotoxins C1 and C2."
 RL Infect. Immun. 57:2249-2252(1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=96027099; PubMed=7582894;
 RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
 RA Brehm R.D., Tranter H.S.;
 RT "Crystal structure of the superantigen enterotoxin C2 from
 RT Staphylococcus aureus reveals a zinc-binding site."
 RL Structure 3:769-779(1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F., Jr., Fletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 RT enterotoxins."
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN [4]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=9734373; PubMed=9191070;
 RA Schod E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 RT enterotoxins A and C2 reveals remarkable similarity and
 RT dissimilarity."
 RL J. Mol. Biol. 269:270-280(1997).
 CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 CC for the toxin interaction with MHC class II.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
 CC PIR: A60114; A60114.
 DR PDB: 1STE; 23-DEC-96.
 DR PDB: 1SE2; 08-MAR-96.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_Strep_toxin_1.
 DR Pfam: PF02876; Staph_Strep_toxin_C_1.
 DR PRINTS: PR00279; BACTRITOXIN.
 DR PROSITE: PS00277; STAPH-STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH-STREP_TOXIN_2; 1.
 DR Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; zinc;
 KW 3D-structure.
 FT SIGNAL 1 27
 FT CHAIN 28 266 ENTEROTOXIN TYPE C-2.
 FT DISULFID 120 137

FT METAL 36 36 ZINC.
 FT METAL 110 110 ZINC.
 FT METAL 145 145 ZINC.
 FT METAL 149 149 ZINC.
 SQ SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;
 Query Match 41.5%; Score 549; DB 1; Length 266;
 Best Local Similarity 44.1%; Pred. No. 9,26-35;
 Matches 113; Conservative 52; Mismatches 73; Indels 18; Gaps 8;

QY 11 MVF-FVLYTFGLTISOEVRQADPPDSQHRSS-LYKNLONITFLYEGDPYIENKSV 68
 DB 12 LIFALILVLFPTPNVLA--SQDPPTDELKHSSEFTGTGMNMYLDDHVSATKWSV 68
 QY 69 DQASHDLIVNSG---PNYDKLTETLKNOMATLFDKNDIVGVEYHLCYAC--ENA 123
 DB 69 DKFLAHLIYNISRKLNKNDKVTLELNEDLAKKYDEYVDYGSNTYVNCYSSKDNV 128
 QY 124 ER---SACIYGVGTNEGHNLKLP--KTIYKVSIDGIOSLSPDIETNKKMYTAQELDY 177
 DB 129 GKVTGKTCMGCGITKEGHNFNGNLQNVLIYREKKNRNTISFEVQTDKSVTAQELDI 188
 QY 178 KVRKYLDNKKOLYTNQPSKYETGYIKFIPKKESEFDFPEP--EFTQSKYLMYKDN 235
 DB 189 KARNFLINKKNLYENSSPYETGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMYKDNK 248
 QY 236 TLDSNTSOIEVYLTK 251
 DB 249 TVDSKSVKIEVHLTK 264

RESULT 5
 ETC1_STAU STANDARD; PRT: 266 AA.
 ID ETC1_STAU STANDARD; PRT: 266 AA.
 AC P01553;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Enterotoxin type C-1 precursor (SEC1).
 GN EMTC1.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_Taxid=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88038352; PubMed=2823067;
 RA Bohach G.A., Schlievert P.M.;
 RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
 RT relatedness to other pyrogenic toxins."
 RL Mol. Gen. Genet. 209:15-20(1987).
 RN [2]
 RP SEQUENCE OF 28-266.
 RX MEDLINE=83213327; PubMed=6189824;
 RA Schmidt J.J., Spero L.;
 RT "The complete amino acid sequence of staphylococcal enterotoxin C1."
 RL J. Biol. Chem. 258:6300-6306(1983).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
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 CC -----
 DR EMBL: X05815; CAA29260.1; -
 DR PIR: A01816; ENSAC1.
 DR PIR: S06356; S06356.

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DR HSP: P34071; 15E2.
DR InterPro: IPR001961; Staph/Strep-toxin.
DR Pfam: PF01123; Staph-Strep-toxin; 1.
DR Pfam: PF02876; Staph-Strep-toxin; 1.
DR PRINTS: PR00279; BACTERIOTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Enterotoxin; Toxin; Signal; Superantigen.
KW SIGNAL
FT CHAIN 1 266 ENTEROTOXIN TYPE C-1.
FT DISULFID 120 137
FT CONFLICT 177 177 D -> N (IN REF. 2)
SQ SEQUENCE 266 AA; 30546 MW; 3A7AB3A8986538 CRC64;

Query Match
Best Local Similarity 41.5%; Score 548; DB 1; Length 266;
Matches 114; Conservative 51; Mismatches 73; Indels 18; Gaps 8;

QY 11 MFF-FLVYFLGLTISOEFVFAQDDPPQSLHSSLVKNL-QNIFYLEGDPVTHENKVS
DB 12 LIFALLVLETPNVLAE--SQDPPDELHRAKSKFTGLMKNKVLVDHYVSATKVS
QY 69 DOLRSHDLIYNVSG--PNYDKLTLELNQEMATLFDKNDVIGVEYTHLCYLC--ENA 123
DB 69 DKFLADLIYNISDKLKNYDKVKTLLNEGLAKKXKDEVVDYGSNYYVNCYFSSKQNV 128
QY 124 ER---SACIYGVGTNHEGNNLEIP--KRIYKVSIDGIQSLSPDIETNKKMYTAQELDY 177
DB 129 GKVTGKTCMYGGITKEHNEHFNMGNIQVLLIRVYENKNNTISFEVOTRKKSVAQELDI 188
QY 178 KVKKYLTDNKKOLYTNPSKYETGYIKFKIKNKSEFWEDEFPPE--EFTOSKYLIMTKDNE 235
DB 189 KANFLINKNKLLEFNSSPEETGYIKFLENNGNTFWYDMPAPGDFDQSKILMAYNDK 248
QY 236 TLDSTNSOLEVYLT 251
DB 249 TVDSKSVKIEVHLTK 264

RESULT 6
ETXG_STAM STANDARD; PRT; 258 AA.
ID ETXG_STAM
AC 085382;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Enterotoxin type G precursor (SEG).
GN EMWG OR SEG OR SAVI824 OR SA1642.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879, 1280;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-FR1572;
RA MEDLINE=98298056; PubMed=9632603;
RA Munson S.H., Tremaine M.T., Beasley M.J., Welch R.A.;
RT "Identification and characterization of staphylococcal enterotoxin
RL types G and I from Staphylococcus aureus."
RL Infect. Immun. 66:3337-3348(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Mu50 / ATCC 700699, and N315;
RC MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Ihan J.-O., Ito T.,
RA Kamamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani Y., Takahashi N.K., Sawano T., Inoue S.-T., Kaito C.,
RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratsuki K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus

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FT aureus".
RL Lancet 357:1225-1240(2001).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
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CC or send an email to license@sib-sib.ch).
CC -----
CC DR EMBL; AF064773; AAC26660.1; -
CC DR EMBL; AP003363; BAB57986.1; -
CC DR EMBL; AP003135; BAB42910.1; -
CC DR HSP: P01552; 1SBB.
CC DR InterPro: IPR001961; Staph/Strep-toxin.
CC DR Pfam: PF01123; Staph-Strep-toxin; 1.
CC DR Pfam: PF02876; Staph-Strep-toxin; 1.
CC DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
CC DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
CC KW Enterotoxin; Toxin; Signal; Superantigen; Complete proteome.
FT SIGNAL 1 25
FT CHAIN 26 258 ENTEROTOXIN TYPE G.
FT DISULFID 116 133 BY SIMILARITY.
SQ SEQUENCE 258 AA; 29940 MW; E2982101701D012C CRC64;

Query Match
Best Local Similarity 36.4%; Score 481; DB 1; Length 258;
Matches 105; Conservative 46; Mismatches 91; Indels 16; Gaps 5;

QY 8 LKKWFFVLYFLGLTISOEFVFAQDDPPD--SQLHSSLVKNL---LQNIIFYLEGDPVT 61
DB 1 MKKLSVLIILILEIFVFNHMYVNAQPPDKDELKVDSDYKNNKCTMGNVNMLYTSPEVE 60
QY 62 HENKVSVOQLRSHDLIYNVSGNYGNYDKLTLELNQEMATLFDKNDVIGVEYTHLCYLC 121
DB 61 GGVVINSQFSLHDLIFLEYKSYNEVKTELENNANNYDKKVDYGVPPFYCIIPK 120
QY 122 NAE-----RSACIYGVGTNHEGNNLEIPKRIYKVSIDGIQSLSPDIETNKKMYTAQEL 175
DB 121 SEDPINQNGCGCGMGGLFNSEN-ERDKLTGVYTDNRQSLGFTITNNMYTIOEL 179
QY 176 DYKVRKYLTDNKKOLYTNPSKYETGYIKFKIKNKSEFWEDEFPPE--EFTOSKYLIMTK 232
DB 180 DYKARHMLTKREKKLYEFDGSAFESGYIKFKTEKNNTSPWFLPKKELVPEVPYKFLNITG 239
QY 233 DNETLSTNSOLEVYLT 250
DB 240 DNKVDKSKIKMEVFLNT 257

RESULT 7
ETXG_STAM STANDARD; PRT; 258 AA.
ID ETXG_STAM
AC P20723;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Enterotoxin type D precursor (SBD).
GN EMTD.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89359112; PubMed=2549000;
RA Bayles K.W., Iandolo J.J.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal

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RT enterotoxin D.*;
RL J. Bacteriol. 171:4799-4806(1989).
RN [2]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC STRAIN-ATCC 23235;
RX MEDLINE-97157473; PubMed-9003758;
RA Sundelstem M., Abrahamson L., Antonsson P., Mehndate K., Mourad W.,
  Dahlsten M.;
RT "The crystal structure of staphylococcal enterotoxin type D reveals
  Zn2+-mediated homodimerization."
RL EMBO J. 15:6837-6840(1996).
CC -1- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
  STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
  FAMILY.
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CC -----
DR EMBL: M28521; AAB06195.1; -.
DR PIR: A33953; A33953.
DR HSSP: P13163; 1SXT.
DR InterPro: IPR001961; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_Strep_tox_C; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRILTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Zinc.
FT SIGNAL 1 25
FT CHAIN 26 258 ENTEROTOXIN TYPE D.
FT METAL 212 212 ZINC.
FT METAL 250 250 ZINC.
FT METAL 252 252 ZINC.
FT METAL 114 114 ZINC.
FT VARIANT 114 114 P -> A (IN STRAIN ATCC 23235).
SQ SEQUENCE 258 AA; 29746 MM; 4F7C6A2BD42597FD C6C64;

Query Match 25.7%; Score 340; DB 1; Length 258;
Best Local Similarity 35.2%; Pred. No. 5.9e-19;
Matches 92; Conservative 47; Mismatches 102; Indels 20; Gaps 10;

OY 8 LKRM-VFVLTFLGLTISQ-EVFAQDDP--PSQLHR-----SLVKNLQNIYFLYEG 57
DB 1 MKRNFILIALFLFTSLVISPANVANKENIDSVKKEKELKKSSELSTALNNKHSY--ADK 58
OY 58 DPTVHENVKSVQDLRSHDLIYN--VSGPNYDKLTKELEKQENATLFRKRNVDYGEVY 114
DB 59 NPIIGEMKSTGDOFLNTLLYKKRFTDLINFDLLINFNSEKMAHQHRSKNVDYPIRYS 118
OY 115 HLCYLENERSACIYGVTNHEGNHLEIPKRIYVVSIGIQ-SLSFD-IENKKAVTA 172
DB 119 INCGGE-IDRTACTGVTTPHEGNKIKERKKIPINLIMINGVOKEVSLDVQTDKNVTV 177
OY 173 QELDYKVRKYLTDNKKQLYTNGP--SKYETGYIKFIPKNSKSFDFPEPEFQSKYLM 230
DB 178 QELDAQARYLQDLKLYNNDTLGKIGRKIEFDSDSKVSYDLFDVGDPEPEQLRI 237
OY 231 YKNETLDSNTSQILEVLTTR 251
DB 238 YSDKLTSLTEHLHIDYLYEK 258

RESULT 8
ETXE STRAU
ID ETXE STRAU STANDARD; PRT; 257 AA.
AC P12993;

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DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Enterotoxin type E precursor (SEE).
GN ENTE.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN (1)
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
RC STRAIN-MJB265;
RX MEDLINE-88257005; PubMed-3384800;
RA Couch J.L., Solis M.T., Bettey M.J.;
RT "Cloning and nucleotide sequence of the type E staphylococcal
  enterotoxin gene."
RL J. Bacteriol. 170:2954-2960(1988).
RN (2)
RP 3D-STRUCTURE MODELING.
RX MEDLINE-96022987; PubMed-7552730;
RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
  enterotoxins."
RL Nat. Struct. Biol. 2:680-686(1995).
CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
  for the toxin interaction with MHC class II (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
  STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
  FAMILY.
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CC -----
DR EMBL: M21319; AAB26617.1; -.
DR PIR: A28179; A28179.
DR PDB: 1SEB; 15-OCT-95.
DR InterPro: IPR001961; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRILTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
  3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 257 ENTEROTOXIN TYPE E.
FT METAL 211 211 ZINC (BY SIMILARITY).
FT METAL 249 249 ZINC (BY SIMILARITY).
FT METAL 251 251 ZINC (BY SIMILARITY).
SQ SEQUENCE 257 AA; 29358 MM; 27EDA94B97770CE3 C6C64;

Query Match 23.3%; Score 308; DB 1; Length 257;
Best Local Similarity 32.7%; Pred. No. 1.6e-16;
Matches 86; Conservative 49; Mismatches 98; Indels 30; Gaps 11;

OY 10 KMFVLTFLGLTI-----SQEFAQDDPSPQLHRSSLVKNLQNIYFLYEGD 58
DB 2 KTAFFILFLFIALTTTSPLVNGSEKSEERINKDLRKSELGRNL-SLRQIYV-YNEK 59
OY 59 PYTHENVKSVQDLRSHDLIYN--VSGPNYDKLTKELEKQENATLFRKRNVDYGEVY 115
DB 60 AIT-ENKESDDQFLNTLLFKGFTGHPYNDLVDLSKQATNKKYKQVLYGAYGY 118
OY 116 LCYLENERSACIYGVTNHEGNHLEIPKRIYVVSIGIQ-SLSFD-IENKKAVTA 173
DB 119 QC-AGGTPKTKACMGVTLHNDNNLTREKVPINLMDIGKQTVIPIDKXAKSKEVTV 177

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Oy 174 ELDYKVRKYLTDNKLNTNGP--SKYETGYIKFIPKNNESFDFPEPEFTOSKY----- 227
Db 178 ELDLQARRYLNGKGLYNSDFGCKVQKGLIVFHSSESTVSYDLFD-----AQOQYPTL 233
Oy 228 LMIYKNETLDSNTSQIEVYLT 250
Db 234 LRIYRDNKTINSEMHIDLYLT 256

RESULT 9
ETXA_STAAW STANDARD; PRT; 257 AA.
ID ETXA_STAAW STANDARD; PRT; 257 AA.
AC P13163;
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Enterotoxin type A precursor (SEA).
GN ENTA OR MW1889.
OS Staphylococcus aureus (strain MW2), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620, 1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MW2;
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-FRI337;
RX MEDLINE=88086892; PubMed=3335483;
RA Betley M.J., Mekalanos J.J.;
RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene."
RL J. Bacteriol. 170:34-41(1988).
RN [3]
RP SEQUENCE OF 25-257.
RX MEDLINE=87222293; PubMed=3584106;
RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
RT "Complete amino acid sequence of staphylococcal enterotoxin A."
RL J. Biol. Chem. 262:7006-7013(1987).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95354648; PubMed=7628431;
RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohlisten M., Kalland T.,
RA Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
RT "Crystal structure of the superantigen staphylococcal enterotoxin
RT type A."
RL EMBO J. 14:3292-3301(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=97113025; PubMed=8943278;
RA Sundstroem M., Hallen D., Svensson A., Schad E., Dohlisten M.,
RA Abrahamson L.;
RT "The Co-crystal structure of staphylococcal enterotoxin type A with
RT Zn2+ at 2.7-A resolution. Implications for major histocompatibility
RT complex class II binding."
RL J. Biol. Chem. 271:32212-32216(1996).
RN [6]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins."
RL Nat. Struct. Biol. 2:680-686(1995).
RN [7]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=9734373; PubMed=9191070;
RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;

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RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity."
RL J. Mol. Biol. 269:270-280(1997).
CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC -----
DR EMBL; AP004828; BAB95754.1; -
DR EMBL; M18970; AAA26681.1; -
DR PIR; A28664; A28664.
DR PIR; A29566; A29566.
DR PDB; 1ESF; 1J-JUL-96.
DR PDB; 1SEA; 15-OCT-95.
DR PDB; 1SXT; 19-NOV-97.
DR InterPro; IPR001961; Staph/Strep-toxin.
DR Pfam; PF01123; Staph-Strep-toxin; 1.
DR Pfam; PF02876; Staph-Strep-toxin C; 1.
DR PRINTS; PR00279; BACTERIOTOXIN.
DR PROSITE; PS00277; STAPH-STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH-STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
KW 3D-structure.
FT SIGNAL. 1 24
FT CHAIN. 25 257 ENTEROTOXIN TYPE A.
FT DISULFID 120 130
FT METAL 211 211 ZINC.
FT METAL 249 249 ZINC.
FT METAL 251 251 ZINC.
FT CONFLICT 242 242 T->S (IN REF. 3).
SQ SEQUENCE 257 AA; 29669 MW; ADEBFBSCALF14677 CAC64;

Query Match 23.2%; Score 307; DB 1; Length 257;
Best Local Similarity 30.9%; Pred. No. 1.8e-16;
Matches 80; Conservative 49; Mismatches 108; Indels 22; Gaps 7;

Oy 10 KMVFVLYTFGLTI-----SQEVFAQDDPDSOLHRSSLVENLQNYELYEGD 58
Db 2 KKTAFLLLFALTYLTSPLVNGSEKSEINEKDLRKSELOGTAL-GNLKQIY--YNE 58
Oy 59 PVTENKSVQDLRSHDLIYN---VSGPNYDKLTLELNOEMATFKDKNVDIYGVETYY 115
Db 59 KAKTENKESHQFLOHTILFKGFIFDHSWYNLDLVDPSKDIYDKKQKVDLYAYGY 118
Oy 116 LCYLCEANRSACIYGVYTNHEGNIHLPEKIVKVSIDGIOSL--SFDIETKKNMVTQ 173
Db 119 OC-AGCTPNKTCACMGVTLHDNRLTEKKKPVIMLDGKONTVPLEIVKKNKNVTVQ 177
Oy 174 ELDYKVRKYLTDNKLNTNGP--PSKYETGYIKFIPKNNESFDFPEPEFTOSKYLMY 231
Db 178 ELDLQARRYLNGKGLYNSDFGCKVQKGLIVFHSSESTVSYDLFDGAGOGYSNTLLAY 237
Oy 232 KDNETLDSNTSQIEVYLT 250
Db 238 RDNKTINSEMHIDLYLT 256

RESULT 10
SPEC_STRPY

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ID SPEC_STRPY STANDARD: PRT: 235 AA.
AC P13380:
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Exotoxin type C precursor (SPE C).
GN SPEC OR SPY0711.
OS Streptococcus pyogenes.
OC Bacteria: Firmicutes; Lactobacillales; Streptococcaceae;
CC Streptococcus.
CX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-52.
RC STRAIN-T18P / MGAS 1585;
RX MEDLINE-88314303: PubMed=3045005;
RA Goshorn S.C., Schlievert P.M.;
RL "Nucleotide sequence of streptococcal pyrogenic exotoxin type C.";
RN Infect. Immun. 56:2518-2520(1988).
RN [2]
RP REVISIONS TO 21-26.
RC STRAIN-T18P / MGAS 1585;
RX MEDLINE-92363541: PubMed=1500157;
RA Kapur V., Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RN "Molecular population genetic evidence of horizontal spread of two
alleles of the pyrogenic exotoxin C gene (speC) among pathogenic
clones of Streptococcus pyogenes.";
RL Infect. Immun. 60:3513-3517(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE-21192684: PubMed=11296296;
RA Ferretti J.D., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RN Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RN Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RL "Complete genome sequence of an M1 strain of Streptococcus
pyogenes.";
RN Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-235.
RX MEDLINE-97397352: PubMed=9253413;
RA Roussel A., Anderson B.F., Baker H.M., Fraser J.D., Baker E.N.;
RN "Crystal structure of the streptococcal superantigen SPE-C:
dimerization and zinc binding suggest a novel mode of interaction
with MHC class II molecules.";
RL Nat. Struct. Biol. 4:635-643(1997).
RN [5]
RP SUBUNIT: Binds to major histocompatibility complex class II beta
chain.
RN [6]
RP DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
FEVER.
RN [7]
RP MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
RN [8]
RP SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
FAMILY.
RN [9]
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or send an email to license@isb-sib.ch).
RN [10]
RP EMBL: M35514; AAA27017.1; ALT_SEQ.
RN EMBL: M97156; AAB59091.1;
RN EMBL: M97157; AAB59092.1;
RN EMBL: A8005523; AAK33664.1;
RN FTR: A30509; A30509.
RN PDB: 1AN8; 29-APR-98.
RN InterPro: IPR001961; Staph/Strep-toxin.
RN Pfam: PF01123; Staph_Strep_toxin; 1.

DR Pfam: PF02876; Staph_Strep-toxin; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
RN Toxin: Signal; 3D-structure; Complete proteome.
FT SIGNAL 1 27
FT CHAIN 28 235 EXOTOXIN TYPE C.
FT CONFID 53 53 N -> D (IN REF. 1).
SQ SEQUENCE 235 AA; 27371 MW; 070534ABB952C1E0 CRC64;
Query Match 16.3% Score 215; DB 1; Length 235;
Best Local Similarity 28.2% Pred. No. 1.5e-09; Index 34; Gaps 12;
Matches 72; Conservative 51; Mismatches 98;
QY 5 KYALKKRVFVLVTFGLRTISQEVFAQODPSPQLHRSSLVKMNINIFLYEGDPVTHEN 64
DB 2 KNIINIKIVPIIVILISTISPIKSKDKDISNVK-----SLLVAVITTPDYKN 53
QY 65 VKSVQDLRSHDLVYNSGPNYD---KKTLELNQEMATLFFKKNVDIYGEYHLCLYL 120
DB 54 CR-VNFSSTHTL--NIDTOKYRGKDYISSEMSYEASQKFRKRDHVDVGL-FYIL---- 105
QY 121 ENAERSACIYGVY---NHEGNHLEIPKRIYVVSIDG--IGSLSPDIETNKKMVAQEL 175
DB 106 -NSHTGEYIGGITPAPNNKNVNH-----KLGSLFTSGSQNLNKKIILENDIYVFOE 159
QY 176 DYVKRYITLDNKKOLYNGSPSKYETGYIKFKPKKESFWDFPEP-EFTQSKLYMIYKN 234
DB 160 DFKIRRYLMDNYKIV-DATSPYVSGRIEIGTKGKHQIDLFDSFNEGTRSDIFAKYKN 218
QY 235 ETLID-SNTSIOIEYVL 248
DB 219 RIINMNFHSFDITL 233
RESULT 11
SPEH_STRPY
ID SPEH_STRPY STANDARD: PRT: 236 AA.
AC 09X5C8:
DT 16-OCT-2001 (Rel. 40, Created).
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Exotoxin type H precursor (SPE H).
GN SPEH OR SPY1008.
OS Streptococcus pyogenes.
OC Bacteria: Firmicutes; Lactobacillales; Streptococcaceae;
CC Streptococcus.
CX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RN [2]
RP STRAIN-M15:
RX MEDLINE-99093428: PubMed=9874566;
RA Proft T., Moffatt S.L., Betkahn C.J., Fraser J.D.;
RN "Identification and characterization of novel superantigens from
Streptococcus pyogenes.";
RL J. Exp. Med. 189:89-102(1999).
RN [3]
RP SEQUENCE FROM N.A.
RN [4]
RP STRAIN-SF370 / Serotype M1;
RX MEDLINE-21192684: PubMed=11296296;
RA Ferretti J.D., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RN Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RN Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RL "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RN Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RN [5]
RP SUBUNIT: Binds to major histocompatibility complex class II beta
chain.
RN [6]
RP SUBCELLULAR LOCATION: Secreted.
RN [7]
RP DISEASE: Mitogenic for human peripheral blood lymphocytes.
RN [8]
RP SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
FAMILY.

RA Qian Y., Jia H.-G., Najaf F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.,
RA "Complete genome sequence of an M1 strain of *Streptococcus pyogenes*,"
RA Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -1- SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain.
CC -1- DISEASE: Mitogenic for human peripheral blood lymphocytes.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
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CC or_send_an_email_to_license@sib-sib.ch](http://www.isb-sib.ch/announce/or_send_an_email_to_license@sib-sib.ch)).
CC -----
DR EMBL: AF124499; AAD30988.1; -
DR EMBL: AE006489; AAK33303.1; -
DR HSSP: P13380; 1ANB.
DR InterPro: IPR001961; Strep/Strep_toxin.
DR Pfam: PF01123; Strep_Strep_toxin_1.
DR Pfam: PF02876; Strep_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Signal; Complete proteome.
FT SIGNAL 1 24
FT CHAIN 1 24 POTENTIAL.
FT EXOTOXIN TYPE G.
SQ SEQUENCE 234 AA; 217262 MW; 49525C49E4BA2052 CRC64;
Query Match 12.5%; Score 165; DB 1; Length 234;
Best Local Similarity 25.0%; Pred. No. 9,3e-06;
Matches 55; Conservative 40; Mismatches 81; Indels 44; Gaps 10;
QY 63 ENKVSQVLNSHDLIVVSGPNDK-----LKTELKNQENA----- 98
DB 26 ENLK-DLKRSLRPAYNITPCDENEVEIAEVTNNSHINKKSECLIVDSIVSLGIT 83
QY 99 -TLPRKDNVDIVGEYHYHLCYLCENAMRASCATYGGVYNH--EGNHLEPKRIYKVSIDG 155
DB 84 DQFLKSGKVDVFGFLPYFSPPYDN-----ITGGIKSHNQGK--SLQFVGLMDQG 134
QY 156 IQSL--SFDIETNKWVTAQELDYKRVKRYLLDNKQLYTNQSPKRYETGYIKFIPKNSEFW 213
DB 135 KETYLPESEAVIRKIKQFTLQEPFKIRKFLMEKYNY-DSESRYSQSLATLKDSKHYE 193
QY 214 FDFPEPEE--FTQSKYLIMYKNDNETLDS-NTSQLEYLTT 250
DB 194 VDLFNKDKLLSRDSPFRKRYKDKNFNSEISHPDIYLYKT 233
RESULT 13
TSST STAU ID TSST STAU STANDARD; PRT; 234 AA.
AC P06886;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Toxin shock syndrome toxin-1 precursor (TSST-1).
GN TSST.
OS *Staphylococcus aureus*.
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=87057222; PubMed=3782090;
RA Biomster-Hautmaaa D.A., Kreiswirth B.N., Kornblum J.S., Novick R.P.,
RA Schlievert P.M.;
RT "The nucleotide and partial amino acid sequence of toxic shock
RT syndrome toxin-1,"
RL J. Biol. Chem 261:15783-15786(1986).

RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=94150598; PubMed=8107781;
 RA Acharya K.R., Passalacqua E.F., Jones E.Y., Harlos K., Stuart D.I.,
 RA Brehm R.D., Tranter H.S.;
 RT "Structural basis of superantigen action inferred from crystal
 structure of toxic shock syndrome toxin-1.";
 RL Nature 367:94-97(1994).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=94092653; PubMed=8268150;
 RA Prasad G.S., Earhart C.A., Murray D.L., Novick R.P., Schlivert P.M.,
 RA Ohlendorf D.H.;
 RT "Structure of toxic shock syndrome toxin 1.";
 RL Biochemistry 32:13761-13766(1993).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.07 ANGSTROMS).
 RX MEDLINE=96319751; PubMed=8759320;
 RA Papageorgiou A.C., Brehm R.D., Leonidas D.D., Tranter H.S.,
 RA Acharya K.R.;
 RT "The refined crystal structure of toxic shock syndrome toxin-1 at
 2.07-A resolution.";
 RL J. Mol. Biol. 260:553-569(1996).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
 RX MEDLINE=97337442; PubMed=9194182;
 RA Prasad G.S., Radhakrishnan R., Mitchell D.T., Earhart C.A.,
 RA Dinges M.M., Cook W.J., Schlivert P.M., Ohlendorf D.H.;
 RT "Refined structures of three crystal forms of toxic shock syndrome
 toxin-1 and of a tetramutant with reduced activity.";
 RL Protein Sci. 6:1220-1227(1997).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF MUTANTS.
 RX MEDLINE=98254504; PubMed=9585531;
 RA Earhart C.A., Mitchell D.T., Murray D.L., Pinheiro D.M., Matsumura M.,
 RA Schlivert P.M., Ohlendorf D.H.;
 RT "Structures of five mutants of toxic shock syndrome toxin-1 with
 reduced biological activity.";
 RL Biochemistry 37:7194-7202(1998).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: THIS TOXIN IS RESPONSIBLE FOR THE SYMPTOMS OF TOXIC
 SHOCK SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 FAMILY.
 CC -----
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 CC -----
 DR EMBL, J02615; AAA26682.1; -;
 DR PIR, A24606; XCSASI.
 DR PDB, 2TSS; 24-DEC-97.
 DR PDB, 3TSS; 24-DEC-97.
 DR PDB, 4TSS; 24-DEC-97.
 DR PDB, 5TSS; 24-DEC-97.
 DR PDB, 1Q1L; 12-AUG-97.
 DR PDB, 2Q1L; 12-AUG-97.
 DR PDB, 1AM7; 18-NOV-98.
 DR PDB, 1TS2; 16-DEC-98.
 DR PDB, 1TS3; 16-DEC-98.
 DR PDB, 1TS4; 16-DEC-98.
 DR PDB, 1TS5; 16-DEC-98.
 DR InterPro; IPR001961; Staph/Strep_toxin.
 DR InterPro; IPR003999; Staph_toxin.
 DR Pfam; PF01123; Staph_strep_toxin_1.
 DR Pfam; PF02876; Staph_strep_toxin_C_1.
 DR PRINTS; PR01501; TOXICSTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

KW Toxin: Superantigen; Signal; 3D-structure.
 FT SIGNAL 1 40
 FT CHAIN 41 234
 SQ SEQUENCE 234 AA; 26306 MW; E95789FE9A1D7AB4 CRC64;
 Query Match 8.2%; Score 109; DB 1; Length 234;
 Best local Similarity 23.2%; Pred. No. 0.16;
 Matches 56; Conservative 35; Mismatches 108; Indels 42; Gaps 8;
 QY 4 NKKVLKMWFEVLVTLGLTISOEFVAQDDPDSQLHRSLSK-----NQNTYFLY 55
 DB 2 NKKLL--MNFIVSPILLATTA-----TDFTPVPLSSNQIITAKASTNDNTRKLDWY 53
 QY 56 ESDPVTHEWVKSVDQLRSHDLIYNVSG-----PNYDKLTKELEKNEMATLFDKNY 106
 DB 54 SSGSDFTFNSVDLSIGSKRIKNTDGSISLIIFPSPIYSPATKGEKVDLNTKRRKSG 113
 QY 107 DIVGEVYHLCYLCENASACIYGVVTHGHNHLEIPKKIVKSIDIQS--LSFDIET 165
 DB 114 HTSEGTYIHF-----QISGVYTNH--KLPTPIELPLKVKVHGKDSPLKYGPKF 159
 QY 166 NKKMVTVAQELDYKVRKLTNDKQLYTNGPSKETGYIKFIPKKESEFWDFFPEPEPTOS 225
 DB 160 DKKQLAISTLDFEIRHQLTIGHLYRS--SDKTGVTWKITMNGSITYQSLSKKFEYNT 217
 QY 226 K 226
 DB 218 K 218
 RESULT 14
 USOL_YEAST STANDARD; PRT; 1790 AA.
 ID USOL_YEAST
 DC P25386;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Intracellular protein transport protein USOL.
 GN USOL OR INT1 OR YDL058W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 ON NCBI_Taxid=4932;
 OX 11
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=XS2180-1A;
 RX MEDLINE=91185402; PubMed=2010462;
 RA Nakajima H., Hirata A., Ogawa Y., Yonehara T., Yoda K.,
 RA Yamasaki M.;
 RT "A cytoskeleton-related gene, usol, is required for intracellular
 protein transport in Saccharomyces cerevisiae.";
 RL J. Cell Biol. 113:245-260(1991).
 RN [2]
 RP SEQUENCE OF 782-1790 FROM N.A.
 RA Hostetter M.K., Herman D.O., Bendel C.M., McClellan M., Tao N.,
 RA Kendrick K.E.;
 RT Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-8 FROM N.A.
 RA Bai Y., Symington L.S.;
 RT Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REQUIRED FOR PROTEIN TRANSPORT FROM THE ER TO THE GOLGI
 COMPLEX.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACELLULAR
 MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE
 ER AND THE GOLGI COMPLEX.
 CC -1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED
 OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL
 COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.
 CC -1- SIMILARITY: BELONGS TO THE VDP/USOL/YBL047C FAMILY.
 CC -----
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DR EMBL: X54378; CAA38253.1; -
DR EMBL: L03188; AAB00143.1; -
DR EMBL: U53668; AAB6659.1; -
DR PIR: A38455; A38455.
DR SGD: S0002216; US01.
KW Interpro: IPR002017; Spectrin.
KW Transport; Protein transport; Golgi stack; Cytoskeleton; Coiled coil.
FT DOMAIN 1 724
FT DOMAIN 725 1790 COILED COIL (POTENTIAL).
FT DOMAIN 465 487 CHARGED (HYPER-HYDROPHILIC).
FT DOMAIN 991 1790 DISPENSABLE FOR THE PROTEIN FUNCTION.
FT DOMAIN 1172 1786 ASP/GLU-RICH (ACIDIC).
FT CONFLICT 847 847 G -> E (IN REF. 2).
FT CONFLICT 924 924 V -> K (IN REF. 2).
FT CONFLICT 1253 1319 I -> V (IN REF. 2).
FT CONFLICT 1461 1461 N -> S (IN REF. 2).
FT CONFLICT 1581 1581 G -> S (IN REF. 2).
FT CONFLICT 1600 1600 I -> V (IN REF. 2).
FT CONFLICT 1661 1661 R -> S (IN REF. 2).
FT CONFLICT 1772 1772 D -> DEEDDE (IN REF. 2).
SQ SEQUENCE 1790 AA; 206424 MW; 6CE2B216F9F4818 CRC64;

Query Match 8.0%; Score 105.5; DB 1; Length 1790;
Best Local Similarity 24.1%; Pred. No. 3.6;
Matches 62; Conservative 38; Mismatches 104; Indels 53; Gaps 11;

QY 1 MENNNKVKLVKMFVFLVTLGLTISQVFAQDDPDSQSLRRSL-VKNQNTLYFLYEGD 58
DB 1500 LENSXKMMKMLESTISNETELKSSMETLRKSDKLEQSKSEEDIKNLQH---EKSD 1555
QY 59 PVT--HENYKVDYKRYLNDKOLYTNKSGNYDKLTKLEK-----NOEMATLEKDKNVDI 108
DB 1556 LSRINSEKDEIELEKSKRIEAKSGSELETVQELNNAQEKIRINAEENTYAKSLIEDI 1615
QY 109 YGVVYHLCYLCENAKRSACIYGGVTNHNHGNHLEIPKRYIKVYKSIDGLOSFDIETNKK 168
DB 1616 ER-----ELMKQKQAEI---KSNQEKELTSLRLKELEDELSTQ-----OKA 1654
QY 169 MYTACELDYKVRKRYLNDKOLYTNKSGNYDKLTKLEK-----NOEMATLEKDKNVDI 228
DB 1655 QKSEERRAEVRKFFQVEKSQL-DEKAMLETIKYNDLV--NKEQAW---KRDEDTYVK-- 1705
QY 229 MIYKNETLDSNTSQTE 245
DB 1706 -----TTDSQROQETIE 1715

RESULT 15
DSC1_HUMAN
ID DSC1_HUMAN STANDARD; PRT; 894 AA.
AC 008554;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Desmocollin 1A/1B precursor (Desmosomal glycoprotein 2/3) (DG2/DG3).
GN DSC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE-Foreskin;
RX MEDLINE=93283249; PubMed=8507556;
RA Theis D.G., Koch P.J., Franke W.W.;
RT "Differential synthesis of type 1 and type 2 desmocollin mRNAs in

RT human stratified epithelia.";
RL Int. J. Dev. Biol. 37:101-110(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Foreskin;
RA Zimbelmann R.;
RN Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC TISSUE-Skin;
RX MEDLINE=94116981; PubMed=8288219;
RA King I.A., Arneemann J., Spurr N.K., Buxton R.S.;
RT "Cloning of the cDNA (DSC1) coding for human type 1 desmocollin and
its assignment to chromosome 18.";
RL Genomics 18:185-194(1993).
[4]
RP SEQUENCE OF 135-151 AND 283-292.
RX MEDLINE=91323543; PubMed=1713860;
RA King I.A., Magee A.I., Rees D.A., Buxton R.S.;
RT "Keratinization is associated with the expression of a new protein
related to the desmosomal cadherins Dgit/Iti.";
RL FEBS Lett. 286:9-12(1991).
CC -1- FUNCTION: COMPONENT OF INTERCELLULAR DESMOsome JUNCTIONS. INVOLVED
CC IN THE INTERACTION OF PLAQUE PROTEINS AND INTERMEDIATE FILAMENTS
CC MEDIATING CELL-CELL ADHESION. MAY CONTRIBUTE TO EPIDERMAL CELL
CC POSITONING (STRATIFICATION) BY MEDIATING DIFFERENTIAL
CC ADHESIVENESS BETWEEN CELLS THAT EXPRESS DIFFERENT ISOFORMS. LINKED
CC TO THE KERATINIZATION OF EPITHELIAL TISSUES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1A/DG2 (SHOWN HERE) AND 1B/DG3;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN EPIDERMIS, LESS IN LYMPH
CC NODE AND TONGUE.
CC -1- DOMAIN: CALCIUM MAY BE BOUND BY THE CADHERIN-LIKE REPEATS
CC (POTENTIAL).
CC -1- SIMILARITY: CONTAINS 5 CADHERIN DOMAINS.
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DR EMBL: Z34523; CAA84279.1; -
DR EMBL: Z34522; CAA84278.1; -
DR EMBL: X72925; CAA51428.1; -
DR EMBL: X72925; CAA51429.1; -
DR HSSP: P15116; INCJ.
DR Genew: HGNC:3035; DSC1.
DR MTM: 125643; -
DR Interpro: IPR002126; Cadherin.
DR Pfam: PF00028; cadherin; 5.
DR PRINTS: PR00205; CADHERIN.
DR SMART: SM00112; CA. 5.
DR PROSITE: PS00232; CADHERIN_1; 3.
DR PROSITE: PS00268; CADHERIN_2; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal;
KW Cytoskeleton; Calcium-binding; Alternative splicing.
FT SIGNAL 1 29
FT PROPEP 30 134
FT CHAIN 135 894
FT DOMAIN 135 691
FT TRANSLEM 692 714
FT DOMAIN 715 894
FT DOMAIN 135 242
FT DOMAIN 243 354
FT DOMAIN 355 471
FT DOMAIN 472 575
FT DOMAIN 576 682
FT CARBOHYD 165 165
FT CARBOHYD 546 546

N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

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OM protein - protein search, using sw model

Run on: June 23, 2003, 16:09:16 ; Search time 37.7024 Seconds
(without alignments)
1371.740 Million cell updates/sec

Title: US-10-002-784a-16

Perfect score: 1322
Sequence: 1 MNNKVKLKKWFEVLYTFL.....KDNELTDSNTSQIEVYLTFR 251

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1240	93.8	236	2	P97163	P97163 streptococc
2	1239	93.7	236	2	O54779	O54779 streptococc
3	1234	93.3	236	2	O57453	O57453 streptococc
4	1173	88.7	222	2	O9R931	O9R931 streptococc
5	1109	83.9	236	2	O54696	O54696 streptococc
6	1054	79.7	222	2	O9S524	O9S524 streptococc
7	1054	79.7	222	2	O938P4	O938P4 streptococc
8	555	42.0	271	2	O9R0L6	O9R0L6 staphylococ
9	551	41.7	239	2	O53678	O53678 staphylococ
10	550	41.6	239	2	O06532	O06532 staphylococ
11	549	41.5	239	2	O06533	O06533 staphylococ
12	548	41.5	239	2	O05157	O05157 staphylococ
13	548	41.5	239	2	O06531	O06531 staphylococ
14	544	41.1	239	2	O06535	O06535 staphylococ
15	539	40.8	239	2	O06534	O06534 staphylococ
16	538	40.7	234	2	O9R5X4	O9R5X4 staphylococ

17	536.5	40.6	260	2	O54971	O54971 streptococc
18	531.5	40.2	260	2	O54739	O54739 streptococc
19	531.5	40.2	260	2	O54738	O54738 streptococc
20	512.5	38.8	259	2	O936G4	O936G4 staphylococ
21	481	36.4	258	16	O85382	O85382 staphylococ
22	471	35.6	258	2	O92NF2	O92NF2 staphylococ
23	471	35.6	258	2	O9EZM3	O9EZM3 staphylococ
24	469	35.5	233	2	O8RR77	O8RR77 staphylococ
25	339.5	25.7	261	2	O9EZM8	O9EZM8 staphylococ
26	338	25.6	260	16	O99T46	O99T46 staphylococ
27	337	25.5	136	16	O99T49	O99T49 staphylococ
28	336	25.4	260	16	O99EZU3	O99EZU3 staphylococ
29	311.5	23.6	258	16	O9EZM4	O9EZM4 staphylococ
30	307.5	23.3	241	2	O53585	O53585 staphylococ
31	307	23.2	260	16	O931M4	O931M4 staphylococ
32	305.5	23.1	240	16	O9F0L7	O9F0L7 staphylococ
33	299.5	22.7	268	2	O85217	O85217 staphylococ
34	290.5	22.0	217	2	O8RR76	O8RR76 staphylococ
35	285.5	21.6	108	2	O9EZM5	O9EZM5 staphylococ
36	264	20.0	239	16	O99T47	O99T47 staphylococ
37	263	19.9	239	2	O9EZM7	O9EZM7 staphylococ
38	252.5	19.1	242	2	O54476	O54476 staphylococ
39	251.5	19.0	242	16	O85383	O85383 staphylococ
40	250.5	18.9	242	2	O93CC5	O93CC5 staphylococ
41	246.5	18.6	256	2	O8VLM7	O8VLM7 staphylococ
42	245.5	18.6	242	2	O93CC6	O93CC6 staphylococ
43	231.5	17.5	218	2	O8RR75	O8RR75 staphylococ
44	226.5	17.1	225	2	O9L921	O9L921 streptococc
45	226.5	17.1	225	2	O8VVM1	O8VVM1 streptococc

ALIGNMENTS

RESULT 1
P97163 PRELIMINARY; PRT; 236 AA.
ID P97163; P97164;
AC P97163; P97164;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
BT Type A exotoxin precursor (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxId=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156, AND MGAS500;
RX MEDLINE-92044323; PubMed-1940804;
RA Nelson K., Schlievert P.M., Selaender R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
Streptococcus pyogenes.";
RT J. Exp. Med. 174:1271-1274(1991).
RL
DR EMBL: X61556; CAA43754.1; -
DR EMBL: X61557; CAA43755.1; -
DR EMBL: X61560; CAA43758.1; -
DR EMBL: X61558; CAA43753.1; -
DR EMBL: X61559; CAA43756.1; -
DR EMBL: X61554; CAA43757.1; -
DR HSSP: P08095; 1B12.
DR InterPro: IPR001961; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER
FT SIGNAL <1 22 POTENTIAL.

FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA: 27454 MW: 3FB3F41ABDC13A64 CRC64;
Query Match 93.8%; Score 1240; DB 2; Length 236;
Best Local Similarity 99.6%; Pred. No. 4e-81;
Matches 236; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 KKWVFLVYFLGLTISQEVFAQDDPPSOLHRSLSLVKNLQNTLYELKESGDPVTHENKSV 68
DB 1 KKWVFLVYFLGLTISQEVFAQDDPPSOLHRSLSLVKNLQNTLYELKESGDPVTHENKSV 60
QY 69 DQLRSHDLIYVSGPNYDKLTTELKQEMATLFFDKKNVDIYGEVYHLCTYLCENASRSAC 128
DB 61 DQLRSHDLIYVSGPNYDKLTTELKQEMATLFFDKKNVDIYGEVYHLCTYLCENASRSAC 120
QY 129 IYGVTHHEGNHLEIPKRIYKVSIDGQSLSFDEINKKKMTAQLDYKRYKLTDNKQ 188
DB 121 IYGVTHHEGNHLEIPKRIYKVSIDGQSLSFDEINKKKMTAQLDYKRYKLTDNKQ 180
QY 189 IYGVTHHEGNHLEIPKRIYKVSIDGQSLSFDEINKKKMTAQLDYKRYKLTDNKQ 244
DB 181 IYGVTHHEGNHLEIPKRIYKVSIDGQSLSFDEINKKKMTAQLDYKRYKLTDNKQ 236
- RESULT 2
ID 054779 PRELIMINARY: PRT: 236 AA.
AC 054779: 054736; 054740; 054741;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN 1)
RC SEQUENCE FROM N.A.
RC STRAIN-MGAS624 AND MGAS158 AND MGAS485 AND MGAS491, AND MGAS495;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.";
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL: X61569; CAA43767.1; -;
DR EMBL: X61572; CAA43770.1; -;
DR EMBL: X61568; CAA43766.1; -;
DR EMBL: X61570; CAA43768.1; -;
DR EMBL: X61571; CAA43769.1; -;
DR HSSP: P08095; 1B1Z.
DR InterPro: IPR001961; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_toxin; 1.
DR Pfam: PF02876; Staph_toxin; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA: 27468 MW: 29DF2AD575623A84 CRC64;
Query Match 93.7%; Score 1239; DB 2; Length 236;
Best Local Similarity 99.2%; Pred. No. 4.7e-81;
Matches 234; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 9 KKWVFLVYFLGLTISQEVFAQDDPPSOLHRSLSLVKNLQNTLYELKESGDPVTHENKSV 68
DB 1 KKWVFLVYFLGLTISQEVFAQDDPPSOLHRSLSLVKNLQNTLYELKESGDPVTHENKSV 60

QY 69 DQLRSHDLIYVSGPNYDKLTTELKQEMATLFFDKKNVDIYGEVYHLCTYLCENASRSAC 128
DB 61 DQLRSHDLIYVSGPNYDKLTTELKQEMATLFFDKKNVDIYGEVYHLCTYLCENASRSAC 120
QY 129 IYGVTHHEGNHLEIPKRIYKVSIDGQSLSFDEINKKKMTAQLDYKRYKLTDNKQ 188
DB 121 IYGVTHHEGNHLEIPKRIYKVSIDGQSLSFDEINKKKMTAQLDYKRYKLTDNKQ 180
QY 189 IYGVTHHEGNHLEIPKRIYKVSIDGQSLSFDEINKKKMTAQLDYKRYKLTDNKQ 244
DB 181 IYGVTHHEGNHLEIPKRIYKVSIDGQSLSFDEINKKKMTAQLDYKRYKLTDNKQ 236
- RESULT 3
ID 057453 PRELIMINARY: PRT: 236 AA.
AC 057453:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN 1)
RC SEQUENCE FROM N.A.
RC STRAIN-MGAS496;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.";
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL: X61562; CAA43760.1; -;
DR EMBL: X61563; CAA43761.1; -;
DR EMBL: X61567; CAA43765.1; -;
DR EMBL: X61561; CAA43759.1; -;
DR EMBL: X61564; CAA43762.1; -;
DR EMBL: X61565; CAA43763.1; -;
DR EMBL: X61566; CAA43764.1; -;
DR HSSP: P08095; 1B1Z.
DR InterPro: IPR001961; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_toxin; 1.
DR Pfam: PF02876; Staph_toxin; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA: 27484 MW: 2EF7F41AAC853600 CRC64;
Query Match 93.3%; Score 1234; DB 2; Length 236;
Best Local Similarity 99.2%; Pred. No. 1.1e-80;
Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 9 KKWVFLVYFLGLTISQEVFAQDDPPSOLHRSLSLVKNLQNTLYELKESGDPVTHENKSV 68
DB 1 KKWVFLVYFLGLTISQEVFAQDDPPSOLHRSLSLVKNLQNTLYELKESGDPVTHENKSV 60
QY 69 DQLRSHDLIYVSGPNYDKLTTELKQEMATLFFDKKNVDIYGEVYHLCTYLCENASRSAC 128
DB 61 DQLRSHDLIYVSGPNYDKLTTELKQEMATLFFDKKNVDIYGEVYHLCTYLCENASRSAC 120
QY 129 IYGVTHHEGNHLEIPKRIYKVSIDGQSLSFDEINKKKMTAQLDYKRYKLTDNKQ 188
DB 121 IYGVTHHEGNHLEIPKRIYKVSIDGQSLSFDEINKKKMTAQLDYKRYKLTDNKQ 180

OY 169 LTNGPSKYETGYIKFIPKNKESFWDFPEPTOSKYLMIYKNDNETLDSNTSOI 244
 DB 181 LTNGPSKYETGYIKFIPKNKESFWDFPEPTOSKYLMIYKNDNETLDSNTSOI 236

RESULT 4

OY 09R931 PRELIMINARY: PRT: 222 AA.

AC 09R931: 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Exotoxin A (Fragment).
 GN SPEA.

OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 NCBI_TaxID=1314;

RN [1]
 RC SEQUENCE FROM N.A.

RX MEDLINE-99137798; PubMed-9952369;
 RA Bessen D.E., Izzo M.W., Florentino T.R., Carlingal R.M.,
 RA Hollingshead S.K., Beall B.;
 RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
 tropism in group A streptococci.";
 RT J. Infect. Dis. 179:627-636(1999).

RL EMBL: AF055698; AAD11624.1; -.
 DR HSSP: P08095; 1B12.
 DR InterPro: IPR001961; Strep/Strep_toxin.
 DR Pfam: PF01123; Strep_toxin; 1.
 DR Pfam: PF02876; Strep_toxin; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1
 FT SEQUENCE 222 AA; 25759 MW; 488B7ADCCD91FBA3 CRC64;

Query Match 88.7%; Score 1173; DB 2; Length 222;
 Best Local Similarity 99.5%; Pred. No. 2.2e-76;
 Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 21 GLTISQEVFAQDDPPSQLRHSSLYKLNQNIYFLYEGDPVTHENVKSVDDLRSHDLIYNV 80
 DB 1 GLTISOEVFAQDDPPSQLRHSSLYKLNQNIYFLYEGDPVTHENVKSVDDLRSHDLIYNV 60
 OY 81 SGPVNDKLTETLKNQEMATLFRKNDVIYGVYHLCYCENASRSACIYGVYTHBGNH 140
 DB 61 SGPVNDKLTETLKNQEMATLFRKNDVIYGVYHLCYCENASRSACIYGVYTHBGNH 120
 OY 141 LEIPKRIYKVSIDIGISLSPDIETNKKMVTAGELDYKRYKLTLDNKKQLYTNGSKYETG 200
 DB 121 LEIPKRIYKVSIDIGISLSPDIETNKKMVTAGELDYKRYKLTLDNKKQLYTNGSKYETG 180
 OY 201 YIKETPKKESFWDFPEPTOSKYLMIYKNDNETLDSNTS 242
 DB 181 YIKETPKKESFWDFPEPTOSKYLMIYKNDNETLDSNTS 222

RESULT 5

OY 054696 PRELIMINARY: PRT: 236 AA.

AC 054696: 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Type A exotoxin precursor (Fragment).
 GN SPEA.

OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 NCBI_TaxID=1314;

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-MGAS156;
 RX MEDLINE-92044323; PubMed-1940804;
 RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
 RT "Characterization and clonal distribution of four alleles of the speA
 gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
 Streptococcus pyogenes.";
 RT J. Exp. Med. 174:1271-1274(1991).

RL EMBL: X61573; CAA43771.1; -.
 DR HSSP: P08095; 1B12.
 DR InterPro: IPR001961; Strep/Strep_toxin.
 DR Pfam: PF01123; Strep_toxin; 1.
 DR Pfam: PF02876; Strep_toxin; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1
 FT SIGNAL 1
 FT CHAIN 22
 FT NON_TER 23
 FT SEQUENCE 236 AA; 27575 MW; 70F54120E79127DF CRC64;

Query Match 83.9%; Score 1109; DB 2; Length 236;
 Best Local Similarity 88.6%; Pred. No. 8.9e-72;
 Matches 209; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

OY 9 KKMFEVLVTEGLTISOEVFAQDDPPSQLRHSSLYKLNQNIYFLYEGDPVTHENVKSV 68
 DB 1 KRIYFVLAIFLGLTISOEVFAQDDPPSQLRHSSLYKLNQNIYFLYEGDPVTHENVKSV 60
 OY 69 DOLRSHDLIYNVSGPNYKLTETLKNQEMATLFRKNDVIYGVYHLCYCENASRSAC 128
 DB 61 DOLRSHDLIYNVSGPNYKLTETLKNQEMATLFRKNDVIYGVYHLCYCENASRSAC 120
 OY 129 IYGVYTHBGNHLEIPKRIYKVSIDIGISLSPDIETNKKMVTAGELDYKRYKLTLDNKKQ 188
 DB 121 IYGVYTHBGNHLEIPKRIYKVSIDIGISLSPDIETNKKMVTAGELDYKRYKLTLDNKKQ 180
 OY 189 LTNGPSKYETGYIKFIPKNKESFWDFPEPTOSKYLMIYKNDNETLDSNTSOI 244
 DB 181 LTNGPSKYETGYIKFIPKNKESFWDFPEPTOSKYLMIYKNDNETLDSNTSOI 236

RESULT 6

OY 09S524 PRELIMINARY: PRT: 222 AA.

AC 09S524: 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Exotoxin type A (Fragment).
 GN SPEA.

OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 NCBI_TaxID=1314;

RN [1]
 RC SEQUENCE FROM N.A.

RX MEDLINE-99137798; PubMed-9952369;
 RA Bessen D.E., Izzo M.W., Florentino T.R., Carlingal R.M.,
 RA Hollingshead S.K., Beall B.;
 RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
 tropism in group A streptococci.";
 RT J. Infect. Dis. 179:627-636(1999).

RL EMBL: AF029051; AAD21315.1; -.
 DR HSSP: P08095; 1B12.
 DR InterPro: IPR001961; Strep/Strep_toxin.
 DR Pfam: PF01123; Strep_toxin; 1.
 DR Pfam: PF02876; Strep_toxin; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.

DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON-TER 1
 FT NON-TER 222
 FT NON-TER 23684
 SQ SEQUENCE 222 AA; 23684 MW; 121F846092818F8 CRC64;

Query Match 79.7%; Score 1054; DB 2; Length 222;
 Best Local Similarity 89.2%; Pred. No. 7e-68;
 Matches 198; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 21 GLTISOEVFAOQDPDSQHLRSSLVKNLNIYFLYEGDPVTHENKSVQDLRSHDLIYV 80
 DB 1 GLTISOEVFAOQDPDSQHLRSSLVKNLNIYFLYEGDPVTHENKSVQDLRSHDLIYV 60
 QY 81 SGPNYDKLTLELNQEMATLFKDNVDIYGEYHLCYCEAHERSACTYGGVTNHEGNH 140
 DB 61 SGLNYDKLTLELNQEMATLFKDNVDIYGEYHLCYCEAHERSACTYGGVTNHEGNH 120
 QY 141 LEIPKRIYKVSIDGIQSLSFDIETNKKKMTAQLDYKVRKYLTDNKKLYTNGPSKYETG 200
 DB 121 LEIPKRIYKVSIDGIQSLSFDIETNKKKMTAQLDYKVRKYLTDNKKLYTNGPSKYETG 180
 QY 201 YIKFIPKNESEFDFPEPEFOSKYLIMYKDNETLDSNTS 242
 DB 181 YIKFISKDKETFMDFPEPEFNOVKYILMITYKDNETLDSSTS 222

RESULT 7

QY 0938P4 PRELIMINARY; PRT; 222 AA.
 AC 0938P4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Pyrogenic exotoxin A (Fragment).
 GN SPEA.
 OS Streptococcus equisimilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=119602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=4951;
 RA Kalla A., Beesen D.E.;
 RT "Presence of streptococcal pyrogenic exotoxin A and C genes in human
 RT isolates of group G Streptococci";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY049745; AAI06068.1;
 DR InterPro: IPR001961; Scap/Strep_toxin.
 DR Pfam: PF01123; Scap/Strep_toxin; 1.
 DR Pfam: PF02876; Staph_Strep_toxin; 1.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; UNKNOWN_1.
 FT NON-TER 1
 FT NON-TER 222
 FT NON-TER 23684
 SQ SEQUENCE 222 AA; 23684 MW; 121F846092818F8 CRC64;

Query Match 79.7%; Score 1054; DB 2; Length 222;
 Best Local Similarity 89.2%; Pred. No. 7e-68;
 Matches 198; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 21 GLTISOEVFAOQDPDSQHLRSSLVKNLNIYFLYEGDPVTHENKSVQDLRSHDLIYV 80
 DB 1 GLTISOEVFAOQDPDSQHLRSSLVKNLNIYFLYEGDPVTHENKSVQDLRSHDLIYV 60
 QY 81 SGPNYDKLTLELNQEMATLFKDNVDIYGEYHLCYCEAHERSACTYGGVTNHEGNH 140
 DB 61 SGLNYDKLTLELNQEMATLFKDNVDIYGEYHLCYCEAHERSACTYGGVTNHEGNH 120
 QY 141 LEIPKRIYKVSIDGIQSLSFDIETNKKKMTAQLDYKVRKYLTDNKKLYTNGPSKYETG 200
 DB 121 LEIPKRIYKVSIDGIQSLSFDIETNKKKMTAQLDYKVRKYLTDNKKLYTNGPSKYETG 180

QY 201 YIKFIPKNESEFDFPEPEFOSKYLIMYKDNETLDSNTS 242
 DB 181 YIKFISKDKETFMDFPEPEFNOVKYILMITYKDNETLDSSTS 222

RESULT 8

QY 09F0L6 PRELIMINARY; PRT; 271 AA.
 AC 09F0L6;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Staphylococcal enterotoxin C-bovine.
 GN SEC-BOV.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20566668; PubMed=11114901;
 RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
 RA Meaney W.J., Smyth C.J.;
 RT "Characterization of a putative pathogenicity island from bovine
 RT Staphylococcus aureus encoding multiple superantigens";
 RL J. Bacteriol. 183:63-70(2001).
 DR EMBL: AF217235; AAG29599.1;
 DR HSSP: P34071; ISE2.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_Strep_toxin; 1.
 DR Pfam: PF02876; Staph_Strep_toxin; 1.
 DR PRINTS: PR00279; BACTRILTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 SQ SEQUENCE 271 AA; 31267 MW; 3493F6228B042P10 CRC64;

Query Match 42.0%; Score 553; DB 2; Length 271;
 Best Local Similarity 44.9%; Pred. No. 3.6e-32;
 Matches 115; Conservative 51; Mismatches 72; Indels 18; Gaps 8;

QY 11 MWF-FVLTVELGLTISOEVFAOQDPDSQHLRSSLVKNL-NIYFLYEGDPVTHENKSV 68
 DB 17 LIFALIVLFTPNVLAEE--SQPDPPTDELHKASKFTGLMEMKMLYDRIYSAKKVASV 73
 QY 69 DOLRSHDLIYVSG--PYVDKLTLELNQEMATLFKDNVDIYGEYHLCYLC--ENA 123
 DB 74 DFLAHDLIYVNSDKKLNVDKVTLELNEDLAKRYKDEVDYVGSNYVNCYFSSKDNV 133
 QY 124 ER---SACTYGGVTNHEGNHLEIPK--KIYKVSIDGIQSLSFDIETNKKKMTAQLDY 177
 DB 134 GVTGKTCMYGKIKHGNHNDCKLQNVILIRYENKRNITSEVQIDKKSVAQELDI 193
 QY 178 KVRKYLTDNKKLYTNGPSKYETGYIKFIPKNESEFDFPEPE--EFTQSKYLIMYKDN 235
 DB 194 KARNFLINKNLNLEPNSSPYEGYIKFLENNGNTFMVDMAPQDKFSKYLIMYDNK 253

QY 236 TLDNSTQIEVYLTTK 251

DB 254 TVDSKSVKIEVHLTK 269

RESULT 9

QY 053678 PRELIMINARY; PRT; 239 AA.
 AC 053678;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Enterotoxin (Fragment).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Staphylococcus.
 OX NCBI_TaxID=1280;

OY 30 AQQQDBDSQLHRSS-LYKNIQNITYFLEGDPVTHENAKSVOLRSHDLIYNAGS---PNY 85
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 2 SQPPTPELHRSSEFTGTGMKNKYDYDDHYVSATVKVCDFEHLHDILINIISDOKLKNTY 61
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 86 DKLTLELNQMAMLFROKDNDIVGEVEYYHTLCG--EAER----SACITGGVTNHEGN 139
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 62 DKVTELLNEEDLAKKYEVDVVGYGSNYNCFFSKDNVGKVTNGGKTCTMGGITKHCGN 121
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 140 HLELP--KIIVAKYSINGIOSLSFDIEFNKMVAOELDYRVRRYLTDNNKOLYTNPBSKY 197
 | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

Db 122 HFDNGNLQNLVIRYENKRNRTISFEVOTDKKSVTAQELDIKARFLINKKLYEFNSPY 181
 QY 198 ETGYIKFIKPKKSEFWDFPEP--EFTQSKYLMYKNDNETLDSNTSOIEVYLTTK 251
 Db 182 ETGYIKFIENNGNFWDMMPAPGDKFDQSKYLMYKNDKTVDSKRVKIEVHLTTK 237

RESULT 12

005157 PRELIMINARY: PRT: 239 AA.
 AC 005157;
 DT 01-JUL-1997 (TREMblrel. 04, Created)
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Type C enterotoxin (Fragment).
 OS Staphylococcus intermedius.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Staphylococcus.
 OX NCBI_TaxID=1285;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=95-011195;
 RA Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,
 RA Berger P.H., Kapur V., Stauffer C.V., Bohach G.A.;
 RT "Characterization of the type C enterotoxin (SEC-canine) produced by
 Staphylococcus intermedius pyoderma isolates."
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U91526; AAB50248.1; -
 DR HSSP: P23313; IJCK.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_Strep_toxin; 1.
 DR Pfam: PF02876; Staph_Strep_toxin; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR NON_TER 1
 FT SEQUENCE 239 AA; 27536 MW; D660644660DE4191 CRC64;

Query Match 41.5%; Score 548; DB 2; Length 239;
 Best Local Similarity 47.5%; Pred. No. 9.9e-32;
 Matches 112; Conservative 42; Mismatches 68; Indels 14; Gaps 6;

QY 30 AQQDPDSQHLRSS-LVKNLQNLVIRYENKRNRTISFEVOTDKKSVTAQELDIKARFLINKKLYEFNSPY 85
 Db 2 SQPDPMPDDLKSKSEFETGTGMNKKLYDDVYSATKYKSVKFLAHLDIYINISDKKLKNY 61
 QY 86 DKLTTELKNDMATLFDKNDIYGEVYHLCYLC--ENMR---SACIYGVTNHEGN 139
 Db 62 DKVTELTNEDLAKKYDEVVDYGSNYVNCYFSSKDNQKVTGCTCMGGLTKHEGN 121
 QY 140 HLEIP--KTIYKVSIDGISOISFDIETNKKMTAQLDLYVRKYLTDNKOLYNGPSKY 197
 Db 122 HFDNGNLQNLVIRYENKRNRTISFEVOTDKKSVTAQELDIKARFLINKKLYEFNSPY 181
 QY 198 ETGYIKFIKPKKSEFWDFPEP--EFTQSKYLMYKNDNETLDSNTSOIEVYLTTK 251
 Db 182 ETGYIKFIENNGNFWDMMPAPGDKFDQSKYLMYKNDKTVDSKRVKIEVHLTTK 237

RESULT 13

006531 PRELIMINARY: PRT: 239 AA.
 ID 006531;
 AC 006531;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Enterotoxin type C-4 (SEC4446) (Fragment).
 OS Staphylococcus aureus.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=4446;
 RX MEDLINE=94011313; PubMed=8406814;
 RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 RT biological and evolutionary implications."
 RL Infect. Immun. 61:4254-4262(1993).
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYOGENIC EXOTOXINS ARE ALL RELATED.

DR EMBL: U13374; AAA26618.1; -
 DR HSSP: P34071; ISE2.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_Strep_toxin; 1.
 DR Pfam: PF02876; Staph_Strep_toxin; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Enterotoxin; Toxin; Superantigen.
 FT NON_TER 1
 SO SEQUENCE 239 AA; 27612 MW; BB7BD6204731ED24 CRC64;

Query Match 41.5%; Score 548; DB 2; Length 239;
 Best Local Similarity 47.0%; Pred. No. 9.9e-32;
 Matches 111; Conservative 44; Mismatches 67; Indels 14; Gaps 6;

QY 30 AQQDPDSQHLRSS-LVKNLQNLVIRYENKRNRTISFEVOTDKKSVTAQELDIKARFLINKKLYEFNSPY 85
 Db 2 SQPDPMPDDLKSKSEFETGTGMNKKLYDDVYSATKYKSVKFLAHLDIYINISDKKLKNY 61
 QY 86 DKLTTELKNDMATLFDKNDIYGEVYHLCYLC--ENMR---SACIYGVTNHEGN 139
 Db 62 DKVTELTNEDLAKKYDEVVDYGSNYVNCYFSSKDNQKVTGCTCMGGLTKHEGN 121
 QY 140 HLEIP--KTIYKVSIDGISOISFDIETNKKMTAQLDLYVRKYLTDNKOLYNGPSKY 197
 Db 122 HFDNGNLQNLVIRYENKRNRTISFEVOTDKKSVTAQELDIKARFLINKKLYEFNSPY 181
 QY 198 ETGYIKFIKPKKSEFWDFPEP--EFTQSKYLMYKNDNETLDSNTSOIEVYLTTK 251
 Db 182 ETGYIKFIENNGNFWDMMPAPGDKFDQSKYLMYKNDKTVDSKRVKIEVHLTTK 237

RESULT 14

006535 PRELIMINARY: PRT: 239 AA.
 ID 006535;
 AC 006535;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Enterotoxin type C-3 (SEC3) (Fragment).
 OS Staphylococcus aureus.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRI 909;
 RX MEDLINE=94011313; PubMed=8406814;
 RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 RT biological and evolutionary implications."
 RL Infect. Immun. 61:4254-4262(1993).
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
 CC PYOGENIC EXOTOXINS ARE ALL RELATED.

Search completed: June 23, 2003, 16:14:55
Job time : 40.7024 secs

[illegible]

Query Match	40.8%	Score 539	DB 2:	length 239;
Best Local Similarity	45.8%	Pred. No. 4.3e-31;		
Matches 109; Conservative	48;	Mismatches 63;	Indels 18;	Gaps 6

[illegible]

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 16:10:36 ; Search time 24.0835 Seconds
(without alignments)
2102.722 Million cell updates/sec

Title: US-10-002-784A-27
Perfect score: 2500
Sequence: 1 MOODPDPQLHRSLVKNLQ.....ALGTGGAGGNGYQSAVVG 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues
Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2500	100.0	468	9	US-10-002-784A-27
2	1332	53.3	248	9	Sequence 27, Appl
3	1324.5	53.0	248	9	Sequence 25, Appl
4	1168	46.7	220	9	US-10-002-784A-24
5	1136	45.4	251	1	Sequence 24, Appl
6	1136	45.4	251	1	Sequence 26, Appl
7	1122	44.9	251	8	US-08-882-431-16
8	938.5	37.5	250	9	US-10-002-784A-13
9	543	21.7	239	10	Sequence 16, Appl
10	541	21.6	266	9	US-09-870-759-20
11	539	21.6	266	9	Sequence 12, Appl
12	532	21.3	266	9	US-09-870-759-10
13	530	21.2	239	9	Sequence 10, Appl
14	525	21.0	239	1	US-10-002-784A-6
15	523	20.9	266	1	Sequence 6, Appl
16	514	20.6	266	1	Sequence 10, Appl
17	514	20.6	266	1	US-08-882-431-10
18	513.5	20.5	265	9	Sequence 8, Appl
19	509	20.4	266	9	US-10-002-784A-14
					Sequence 14, Appl
					Sequence 6, Appl
					Sequence 12, Appl

20	506.5	20.3	265	1	US-08-882-431-8	Sequence 8, Appl
21	397.5	15.9	79	9	US-10-002-784A-39	Sequence 39, Appl
22	295.5	11.3	258	9	US-09-870-759-14	Sequence 14, Appl
23	281.5	11.8	217	9	US-09-900-766-6	Sequence 6, Appl
24	263.5	10.5	257	9	US-09-870-759-8	Sequence 8, Appl
25	257.5	10.3	233	9	US-10-002-784A-4	Sequence 4, Appl
26	257.5	10.3	233	9	US-09-900-766-4	Sequence 4, Appl
27	257.5	10.3	233	9	US-10-283-838-7	Sequence 7, Appl
28	257.5	10.3	257	9	US-10-002-784A-2	Sequence 2, Appl
29	256.5	10.3	233	9	US-09-900-766-7	Sequence 7, Appl
30	256.5	10.3	233	9	US-10-283-838-8	Sequence 8, Appl
31	256	10.2	257	1	US-08-882-431-2	Sequence 2, Appl
32	252	10.1	233	1	US-08-882-431-4	Sequence 4, Appl
33	248.5	9.9	203	9	US-09-900-766-5	Sequence 5, Appl
34	244.5	9.8	233	9	US-09-900-766-3	Sequence 3, Appl
35	241.5	9.7	672	9	US-09-900-766-1	Sequence 1, Appl
36	241	9.6	248	9	US-09-870-759-16	Sequence 16, Appl
37	225.5	9.0	233	9	US-09-900-766-2	Sequence 2, Appl
38	188	7.5	89	9	US-10-002-784A-37	Sequence 37, Appl
39	188	7.5	89	9	US-10-002-784A-38	Sequence 38, Appl
40	184	7.4	89	9	US-10-002-784A-36	Sequence 36, Appl
41	156	6.2	89	9	US-10-002-784A-35	Sequence 35, Appl
42	124.5	5.0	82	9	US-10-002-784A-33	Sequence 33, Appl
43	123	4.9	1338	10	US-09-402-100-4	Sequence 4, Appl
44	121.5	4.9	789	9	US-10-099-285-80	Sequence 80, Appl
45	121	4.8	592	10	US-09-765-272-222	Sequence 222, App

ALIGNMENTS

RESULT 1
US-10-002-784A-27
; Sequence 27, Application US/10002784A
; Publication No. US2003003644A1
; GENERAL INFORMATION:
/33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 27
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant SpeA-mutant SpeB fusion
US-10-002-784A-27

Query Match	100.0%	Score	2500;	DB	9;	Length	468;
Best Local Similarity	100.0%	Pred. No.	1.2e-185;				
Matches	468;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	1	MOODPDPQLHRSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLK	60				
Db	1	MOODPDPQLHRSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLK	60				
QY	61	TELKQEMATLFDKRNIDYGVYVYHLCYLCENASACIGVTVNREGNHLBIPKVIYVK	120				
Db	61	TELKQEMATLFDKRNIDYGVYVYHLCYLCENASACIGVTVNREGNHLBIPKVIYVK	120				
QY	121	VSIDIGIQLSPDIENKKNWTAQELDYKVRKYLTNKNOLYTNKPSKYETGYTKFIPKNKE	180				
Db	121	VSIDIGIQLSPDIENKKNWTAQELDYKVRKYLTNKNOLYTNKPSKYETGYTKFIPKNKE	180				
QY	181	SFWEFFPEPEFTQSKYLMYKNDNETLDSNTQIEVYLTTPQPVKSLDSKGIHYNOGNP	240				
Db	181	SFWEFFPEPEFTQSKYLMYKNDNETLDSNTQIEVYLTTPQPVKSLDSKGIHYNOGNP	240				

241	YNLLTPVIEKVKGEQSVFGQHAATGCVATAQAIIMKYHNYPNKGLDKYTYTLSSNNPYF	300
241	YNLLTPVIEKVKGEQSVFGQHAATGCVATAQAIIMKYHNYPNKGLDKYTYTLSSNNPYF	300
301	NHPKNLFAAISTROYNNNNLLPTYSGRESNVQKMAISELMADVGISVDMDYCPSSGSAGS	360
301	NHPKNLFAAISTROYNNNNLLPTYSGRESNVQKMAISELMADVGISVDMDYCPSSGSAGS	360
361	SRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSONQPYVYQGGKVGSGHAFVIDGA	420
361	SRVQRALKENFGYNQSVHQINRSDFSQDWEAQIDKELSONQPYVYQGGKVGSGHAFVIDGA	420
421	DGRNFYHVNHWGCVSDGFFRLDALNPALGTGGGAGFNGYQSAVVG	468
421	DGRNFYHVNHWGCVSDGFFRLDALNPALGTGGGAGFNGYQSAVVG	468

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RESULT 2
US-10-002-784A-25
; Sequence 25, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
;
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 25
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant streptococcal pyrogenic
US-10-002-784A-25

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Query Match	53.3%	Score	1332;	DB	9;	Length	248;
Best Local Similarity	100.0%;	Pred. No.	1.5e-95;				
Matches	248;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
QY	221	QPWVKSLLDSKGIHYNQGNPNYLLTPVIEKVRPGEQSFVQGHAAATGCVATATAQIMKYHN	280				
DB	1	QPWVKSLLDSKGIHYNQGNPNYLLTPVIEKVRPGEQSFVQGHAAATGCVATATAQIMKYHN	60				
QY	281	YPNKGKLDYTYTLSSNNPYFNHPKNLFAAISTROYNNNTLPYSGRESNVQKMAISELM	340				
DB	61	YPNKGKLDYTYTLSSNNPYFNHPKNLFAAISTROYNNNTLPYSGRESNVQKMAISELM	120				
QY	341	ADVGISVDMDYGPSSGSGSSRRVQALKENFGYNQSVHQINRSDFSQDWEAQIDKELSON	400				
DB	121	ADVGISVDMDYGPSSGSGSSRRVQALKENFGYNQSVHQINRSDFSQDWEAQIDKELSON	180				
QY	401	QPYYTQGGKVGGHAFYIDGADGRNFYHVNWGSGVSDGFFRLDALNP SALGTGGGAGGFN	460				
DB	181	QPYYTQGGKVGGHAFYIDGADGRNFYHVNWGSGVSDGFFRLDALNP SALGTGGGAGGFN	240				
QY	461	GTQSAVVG	468				
DB	241	GYQSAVVG	248				

RESULT 3
US-10-002-784A-24
; Sequence 24, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; *12*
; APPLICANT: Ulrich, Robert G.

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; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 24
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin B prosegment
US-10-002-784A-24

Query Match          53.0%; Score 1324.5; DB 9; Length 398;
Best Local Similarity 71.7%; Pred. No. 1..le-94;
Matches 273; Conservative 20; Mismatches 49; Indels 39; Gaps 10;

QY   95 ERSACI--GGVTNREGNHLETPKKIVVKVSDIGISQSLSFDIETNK-KMVTAEQLDYKVRKY 152
      :||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   47 QKSAAIKAGARSAEDIKLD---KVNLGSELSSNMWYCYNLSTGFGFVIVSGDKRSPILGY 103

QY   153 LTDNKLTYNGPSKYETGIYKFTPKKNKESFWDFPEPEPTQSKYLMIYKDNETLDSNTQ 212
      :||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   104 STSG-----SFDANGKENI-----ASPMS-YVEQIKENKKLDT--- 136

QY   213 IEVYLT---KQPVVKSLLDSDKGIHYNQGNPNYLLTPVIEKVKGPGESFVCOHAATGCVA 269
      :||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   137 --TYAGTAETKQPVVKSLLDSDKGIHYNQGNPNYLLTPVIEKVKGPGESFVCGQAATGCVA 194

QY   270 TATAQIMKYHNYPNKGDKDYTTTLSSNNPYNFNHPKNLFAAISTROYNNNLPTYSGRES 329
      :||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   195 TATAQIMKYHNYPNKGDKDYTTTLSSNNPYNFNHPKNLFAAISTROYNNNLPTYSGRES 254

QY   330 NVQKMAISELMADVGISVDMDYGSPSSGAGSSRRVQRALKENFGYNQSVHOINRSDFS-QD 388
      :||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   255 NVQKMAISELMADVGISVDMDYGSPSSGAGSSRRVQRALKENFGYNQSVHOINRGDFSQKD 314

QY   389 WEAQIDKELSONQPVYYQG-GKVGGHAFVIDGADGRNFYHVMGMGVSDGFRLDALNP 447
      :||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   315 WEAQIDKELSONQPVYYQGVGKVGGHAFVIDGADGRNFYHVMGMGVSDGFRLDALNP 374

QY   448 SALGTGGGAGGNGYQSAVVG 468
      :||| ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   375 SALGTGGGAGGNGYQSAVVG 395

RESULT 4
US-10-002-784A-26
Sequence 26, Application US/10002784A
Publication No. US20030036644A1
GENERAL INFORMATION:
/APPLICANT: Ulrich, Robert G.
/TITLE OF INVENTION: Bacterial Superantigen Vaccines
/FILE REFERENCE: 003/233/SAP
/CURRENT APPLICATION NUMBER: US/10/002,784A
/CURRENT FILING DATE: 2001-11-26
/PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
/PRIOR FILING DATE: 97-06-25; 98-09-01
/NUMBER OF SEQ ID NOS: 40
/SOFTWARE: Apple Macintosh Microsoft Word 6.0
/SEQ ID NO 26
/LENGTH: 220
/TYPE: PRT
/ORGANISM: Artificial sequence
/FEATURE:
/OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-A
US-10-002-784A-26

Query Match          46.7%; Score 1168; DB 9; Length 220;
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APPLICANT

Query Match 45.4%; Score 1136; DB 1; Length 251;
Best Local Similarity 98.2%; Pred. No. 2.4e-80;
Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

Db 31 QODPDSQOLHRSSLYVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLKT 90

RESULT 5
US-08-882-431-16
Sequence 16, Application US/08882431
Publication No. US2003009015A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Moran
STREET: US Army MRC -504 Scott Street MCMR-2A (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882.431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 251
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide

Query Match 45.4%; Score 1136; DB 9; Length 251;
Best Local Similarity 98.2%; Pred. No. 2.4e-80;
Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

Db 31 QODPDSQOLHRSSLYVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLKT 90

RESULT 6
US-10-002-784A-16
Sequence 16, Application US/10002784A
Publication No. US2003003644A1
GENERAL INFORMATION:
/33
APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002.784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 16
TYPE: PRP
LENGTH: 251
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant

Query Match 45.4%; Score 1136; DB 9; Length 251;
Best Local Similarity 98.2%; Pred. No. 2.4e-80;
Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

Db 31 QODPDSQOLHRSSLYVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLKT 90

RESULT 7
US-08-973-391A-13
Sequence 13, Application US/08973391A
Patent No. US20020054887A1
GENERAL INFORMATION:
APPLICANT: Schlievert, Patrick M.
APPLICANT: Roggiani, Jennifer
APPLICANT: Stoeht, Jennifer
TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
FILE REFERENCE: 600.311USMO
CURRENT APPLICATION NUMBER: US/08/973.391A
CURRENT FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: PCV/US96/10252
PRIOR FILING DATE: 1996-06-07

Query Match 45.4%; Score 1136; DB 9; Length 251;
Best Local Similarity 98.2%; Pred. No. 2.4e-80;
Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

Db 31 QODPDSQOLHRSSLYVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYVNSGPNYDKLKT 90

PRIOR APPLICATION NUMBER: US 08/480,261
 PRIOR FILING DATE: 1995-06-07
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 13
 LENGTH: 251
 TYPE: PRT
 ORGANISM: Streptococcus pyogenes
 US-08-973-391A-13

Query Match 44.9% Score 1122; DB 8; Length 251;
 Best Local Similarity 97.3%; Pred. No. 2.9e-79;
 Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

OY 2 QODPPSOLHRSRLVKNLQNIYFLYEGDPVTHENKSVQOLRSHDLIYVNSGPNDKLT 61
 DB 31 QODPPSOLHRSRLVKNLQNIYFLYEGDPVTHENKSVQOLRSHDLIYVNSGPNDKLT 90
 OY 62 ELKNOEMATLFKKNIDYGVYHLCYLCENASACI-GGVNREGNHLIPIKTIYVK 120
 DB 91 ELKNOEMATLFKKNIDYGVYHLCYLCENASACIYGVNREGNHLIPIKTIYVK 150
 OY 121 VSDIGQSLSFDIETNKKMTAQLDYKRYKLTNDKOLYTNGPSKYEYIKTIYVK 180
 DB 151 VSDIGQSLSFDIETNKKMTAQLDYKRYKLTNDKOLYTNGPSKYEYIKTIYVK 210
 OY 181 SFMFDFEPPEPTOSKYLMIYKNDLSDNT-QIEVYLTK 220
 DB 211 SFMFDFEPPEPTOSKYLMIYKNDLSDNT-QIEVYLTK 251

RESULT 8
 US-09-870-759-20

Sequence 20, Application US/09870759
 Patent No. US20020177551A1
 GENERAL INFORMATION:
 APPLICANT: TERMAN, David S
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 FILE REFERENCE: 870759
 CURRENT APPLICATION NUMBER: US/09/870,759
 PRIOR FILING DATE: 2002-01-14
 PRIOR APPLICATION NUMBER: US 60/208,128
 PRIOR FILING DATE: 2000-05-30
 NUMBER OF SEQ ID NOS: 166
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 20
 LENGTH: 250
 TYPE: PRT
 ORGANISM: Streptococcus pyogenes
 US-09-870-759-20

Query Match 37.5% Score 938.5; DB 9; Length 250;
 Best Local Similarity 84.9%; Pred. No. 4.7e-65;
 Matches 185; Conservative 5; Mismatches 25; Indels 3; Gaps 3;
 PDDPSOLHRSRLVKNLQNIYFLYEGDPVTHENKSVQOLRSHDLIYVNSGPNDKLT 64
 34 PKPSOQSRNSLVKTFRIYFFMRVLYLTHENKSVQOLRSHDLIYVNSGPNDKLT 93
 65 NOEMATLFKKNIDYGVYHLCYLCENASACI-GGVNREGNHLIPIKTIYVK 123
 94 NOEMATLFKKNIDYGVYHLCYLCENASACIYGVNREGNHLIPIKTIYVK 153
 105 VSDIGQSLSFDIETNKKMTAQLDYKRYKLTNDKOLYTNGPSKYEYIKTIYVK 183
 136 VSDIGQSLSFDIETNKKMTAQLDYKRYKLTNDKOLYTNGPSKYEYIKTIYVK 212
 167 SFMFDFEPPEPTOSKYLMIYKNDLSDNT-QIEVYLTK 220
 198 SFMFDFEPPEPTOSKYLMIYKNDLSDNT-QIEVYLTK 250

US-09-150-947B-12
 Sequence 12, Application US/09150947B
 Patent No. US20020028211A1
 GENERAL INFORMATION:
 APPLICANT: Kaempfer, Raymond
 APPLICANT: Arad, Gila
 TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
 FILE REFERENCE: A31967-PCT-USA-A
 CURRENT APPLICATION NUMBER: US/09/150,947B
 PRIOR FILING DATE: 1998-09-10
 PRIOR APPLICATION NUMBER: PCT/IL97/00438
 PRIOR FILING DATE: 1997-12-30
 PRIOR APPLICATION NUMBER: ISRAEL 119938
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 12
 LENGTH: 239
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 US-09-150-947B-12

Query Match 21.7% Score 543; DB 10; Length 239;
 Best Local Similarity 48.1%; Pred. No. 2e-34;
 Matches 114; Conservative 38; Mismatches 67; Indels 18; Gaps 7;

OY 2 QODPPSOLHRSRLVKNLQNIYFLYEGDPVTHENKSVQOLRSHDLIYVNSGPNDKLT 57
 DB 3 QODPPSOLHRSRLVKNLQNIYFLYEGDPVTHENKSVQOLRSHDLIYVNSGPNDKLT 62
 OY 58 ELKNOEMATLFKKNIDYGVYHLCYLCENASACI-GGVNREGNHLIPIKTIYVK 107
 DB 63 ELKNOEMATLFKKNIDYGVYHLCYLCENASACIYGVNREGNHLIPIKTIYVK 122
 OY 108 GNLHPIPKTIYKVSIDIGQSLSFDIETNKKMTAQLDYKRYKLTNDKOLYTNGPSKY 167
 DB 123 GNLHPIPKTIYKVSIDIGQSLSFDIETNKKMTAQLDYKRYKLTNDKOLYTNGPSKY 182
 OY 166 EFGYIKTIYKVSIDIGQSLSFDIETNKKMTAQLDYKRYKLTNDKOLYTNGPSKY 221
 DB 183 EFGYIKTIYKVSIDIGQSLSFDIETNKKMTAQLDYKRYKLTNDKOLYTNGPSKY 238

RESULT 10
 US-09-870-759-10

Sequence 10, Application US/09870759
 Patent No. US20020177551A1
 GENERAL INFORMATION:
 APPLICANT: TERMAN, David S
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 FILE REFERENCE: 870759
 CURRENT APPLICATION NUMBER: US/09/870,759
 PRIOR FILING DATE: 2002-01-14
 PRIOR APPLICATION NUMBER: US 60/208,128
 PRIOR FILING DATE: 2000-05-30
 NUMBER OF SEQ ID NOS: 166
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 10
 LENGTH: 266
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 US-09-870-759-10

Query Match 21.6% Score 541; DB 9; Length 266;
 Best Local Similarity 47.7%; Pred. No. 3.2e-34;
 Matches 113; Conservative 39; Mismatches 67; Indels 18; Gaps 7;

OY 2 QODPPSOLHRSRLVKNLQNIYFLYEGDPVTHENKSVQOLRSHDLIYVNSGPNDKLT 57
 DB 3 QODPPSOLHRSRLVKNLQNIYFLYEGDPVTHENKSVQOLRSHDLIYVNSGPNDKLT 62
 OY 58 ELKNOEMATLFKKNIDYGVYHLCYLCENASACI-GGVNREGNHLIPIKTIYVK 107
 DB 63 ELKNOEMATLFKKNIDYGVYHLCYLCENASACIYGVNREGNHLIPIKTIYVK 122


```

Db      90  NRVVEFKNDLADKYDKYVDVFGANYVYOCYFSKKTNDINSHQTDKRRKTCMVGVTENH 149
      108  GNLHLEIPKRIYVKSIDQISLFDIETNKKKWTAOELDYKVKRYLTNDKOLYTNGPSKY 167
      150  GNQLDKYSRITVAVFEDGNLISFDVQTNKKVTAOELDYLRHRYLVKNNKLYEFNNSPY 209
QY      168  ETGYIKFIPKNKSEFWDFPEP--EFTQSKYLMIKDNETLDS-NTQIEVYLTTRQ 221
      210  ETGYIKFI-ENENSFYDMMAPAGDKFQDSKTYLMAMNDKMKVDSKDKVIEVYLTTRK 265

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```

RESULT 11
US-10-151-336-8
; Sequence 8, Application US/10151336
; Publication No. US20030079248A1
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh
; APPLICANT: Palmer, Kenneth
; APPLICANT: Hefferton, Kathleen
; APPLICANT: Mor, Tsafir
; APPLICANT: Antzen, Charles
; TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
; FILE REFERENCE: 4868/84453
; CURRENT APPLICATION NUMBER: US/10/151,336
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US/09/414,276
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 266
; TYPE: PRF
; ORGANISM: bean yellow dwarf virus
US-10-151-336-8

```

```

Query Match      21.6%; Score 539; DB 9; Length 266;
Best Local Similarity 47.7%; Pred. No. 4.6e-34;
Matches 113; Conservative 39; Mismatches 67; Indels 18; Gaps 7;

QY      2  OODPDSQLHRSSLYVNTL-ONIFYLEEGDPVTHENKSVQDLRSHDLIYVSGP---NTD 57
      30  QDPDKPDELHKSSKFTGLMKNKVLDDNHVSAINKSIDQSLYFDLISIDTKLGND 89
Db      58  KLTLEKNOEMATLEFDKNIDYGVYHLCYLICENA-----ERSACI-GGYTNR 107
      90  NRVVEFKNDLADKYDKYVDVFGANYVYOCYFSKKTNDINSHQTDKRRKTCMVGVTENH 149
QY      108  GNLHLEIPKRIYVKSIDQISLFDIETNKKKWTAOELDYKVKRYLTNDKOLYTNGPSKY 167
      150  GNQLDKYSRITVAVFEDGNLISFDVQTNKKVTAOELDYLRHRYLVKNNKLYEFNNSPY 209
Db      168  ETGYIKFIPKNKSEFWDFPEP--EFTQSKYLMIKDNETLDS-NTQIEVYLTTRQ 221
      210  ETGYIKFI-ENENSFYDMMAPAGDKFQDSKTYLMAMNDKMKVDSKDKVIEVYLTTRK 265

```

```

RESULT 12
US-10-002-784A-6
; Sequence 6, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 6

```

```

; LENGTH: 266
; TYPE: PRF
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin B
US-10-002-784A-6

```

```

Query Match      21.3%; Score 532; DB 9; Length 266;
Best Local Similarity 46.8%; Pred. No. 1.6e-33;
Matches 111; Conservative 41; Mismatches 67; Indels 18; Gaps 7;

QY      2  OODPDSQLHRSSLYVNTL-ONIFYLEEGDPVTHENKSVQDLRSHDLIYVSGP---NTD 57
      30  QDPDKPDELHKSSKFTGLMKNKVLDDNHVSAINKSIDQSLYFDLISIDTKLGND 89
Db      58  KLTLEKNOEMATLEFDKNIDYGVYHLCYLICENA-----ERSACI-GGYTNR 107
      90  NRVVEFKNDLADKYDKYVDVFGANYVYOCYFSKKTNDINSHQTDKRRKTCMVGVTENH 149
QY      108  GNLHLEIPKRIYVKSIDQISLFDIETNKKKWTAOELDYKVKRYLTNDKOLYTNGPSKY 167
      150  GNQLDKYSRITVAVFEDGNLISFDVQTNKKVTAOELDYLRHRYLVKNNKLYEFNNSPY 209
QY      168  ETGYIKFIPKNKSEFWDFPEP--EFTQSKYLMIKDNETLDS-NTQIEVYLTTRQ 221
      210  ETGYIKFI-ENENSFYDMMAPAGDKFQDSKTYLMAMNDKMKVDSKDKVIEVYLTTRK 265

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RESULT 13
US-10-002-784A-10
; Sequence 10, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 10
; LENGTH: 239
; TYPE: PRF
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin B cytoplasmic
US-10-002-784A-10

```

```

Query Match      21.2%; Score 530; DB 9; Length 239;
Best Local Similarity 47.3%; Pred. No. 2e-33;
Matches 112; Conservative 39; Mismatches 68; Indels 18; Gaps 7;

```

```

QY      2  OODPDSQLHRSSLYVNTL-ONIFYLEEGDPVTHENKSVQDLRSHDLIYVSGP---NTD 57
      30  QDPDKPDELHKSSKFTGLMKNKVLDDNHVSAINKSIDQSLYFDLISIDTKLGND 62
Db      58  KLTLEKNOEMATLEFDKNIDYGVYHLCYLICENA-----ERSACI-GGYTNR 107
      63  NRVVEFKNDLADKYDKYVDVFGANYVYOCYFSKKTNDINSHQTDKRRKTCMVGVTENH 122
QY      108  GNLHLEIPKRIYVKSIDQISLFDIETNKKKWTAOELDYKVKRYLTNDKOLYTNGPSKY 167
      123  GNQLDKYSRITVAVFEDGNLISFDVQTNKKVTAOELDYLRHRYLVKNNKLYEFNNSPY 182
QY      168  ETGYIKFIPKNKSEFWDFPEP--EFTQSKYLMIKDNETLDS-NTQIEVYLTTRQ 221
      183  ETGYIKFI-ENENSFYDMMAPAGDKFQDSKTYLMAMNDKMKVDSKDKVIEVYLTTRK 238

```

RESULT 14

US-08-882-431-10
Sequence 10, Application US/08882431
Publication NO. US20030009015A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Moran
STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-7714
TELEFAX: (301) 619-2065
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 239
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-10

[illegible]

RESULT 15
US-10-002-784A-8
: Sequence 8, Application US/10002784A
: Publication NO. US2003003664A1
: GENERAL INFORMATION:
: /33
: APPLICANT: Ulrich, Robert G.

```

1      TITLE OF INVENTION: Bacterial Superantigen Vaccines
2      FILE REFERENCE: 003/233/SNP
3      CURRENT APPLICATION NUMBER: US/10/002,784A
4      CURRENT FILING DATE: 2001-11-26
5      PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
6      PRIOR FILING DATE: 97-06-25; 98-09-01
7      NUMBER OF SEQ ID NOS: 40
8      SOFTWARE: Apple Macintosh Microsoft Word 6.0
9      SEQ ID NO 8
10     LENGTH: 266
11     TYPE: PRT
12     ORGANISM: Artificial sequence
13     FEATURE:
14     OTHER INFORMATION: mutant staphylococcal enterotoxin B periplasmic
15     US-10-002-784A-8
16
17     Query Match      20.9%; Score 523; DB 9; Length 266;
18     Best Local Similarity 46.8%; Pred. No. 8e-33;
19     Matches 111; Conservative 39; Mismatches 69; Indels 18; Gaps 7.
20
21     QY      2 QDDPDSOLHSSSLVKNL-QNIYFEECDPTHENVKKSVDOILRSHDLIYVSGP---NYD 57
22             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
23     Db      30 QPDPRLDLHSSSKRTGLGMENKKVLYLDNNHNSAIIVKSIDQPRFYDLIYSIMDTLGNND 89
24
25     QY      58 KLKLELKKQENATLEFKDKNNIDLYGYEYVHLCLCENA-----ESASCI-GGVYTRRE 107
26             : : | | | : : | | | : : | | | : : | | | : : | | | : : | | |
27     Db      90 NVRYEEFKKRLDADKKRYDVYEFGANAYVOCASFSKRTNDINSHQTDKRTKMYGGVTEHN 149
28
29     QY      108 GNHLIEPKRIYVKSVIDGISOHSFDETNNKKMVTVAQELDYKRYKYLTDNKKOLYTNGPSKY 167
30             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
31     Db      150 GNQDLKRYSTIVRYVEDEKNNLSPFVQYNNKKVTVQDELIDYLRHLVLYNNKKIYEENNSPY 209
32
33     QY      168 ETGYIKLELPKNKESWFDPFPEP--EFLQSKYILMYKKNELIDS-NTQLEIVLYLTQK 221
34             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
35     Db      210 ETGYIKFL-EENENSTWYDMAPAGCKRFQSKYILMYNDNNKVDASDVAVIEVLYLTQK 265

```

Search completed: June 23, 2003, 16:16:39
Job time : 25.0835 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 16:09:16 ; Search time 70.2976 Seconds
(without alignments)
1371.740 Million cell updates/sec

Title: US-10-002-784a-27

Perfect score: 2500
Sequence: 1 MOODPPSQHRSLSLVKNIQ.....ALGTGAGAGFNGYSAYVG 468

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL.21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1324.5	53.0	398	2	Q9AJD2 streptococc
2	1293.5	51.7	344	2	Q931Q2 streptococc
3	1096.5	43.9	236	2	Q54779 streptococc
4	1095.5	43.8	222	2	Q9R931 streptococc
5	1095.5	43.8	236	2	P97163 streptococc
6	1089.5	43.6	236	2	Q57453 streptococc
7	986.5	39.5	236	2	Q54696 streptococc
8	981.5	39.3	222	2	Q9S524 streptococc
9	981.5	39.3	222	2	Q938P4 streptococc
10	516	20.6	239	2	Q5678 streptococc
11	516	20.6	271	2	Q9F0L6 streptococc
12	515	20.6	239	2	Q06532 streptococc
13	515	20.6	239	2	Q06533 streptococc
14	513	20.5	239	2	Q05157 streptococc
15	513	20.5	239	2	Q06531 streptococc
16	510	20.4	239	2	Q06535 streptococc

17	505	20.2	239	2	Q06534 streptococc
18	504	20.2	234	2	Q9R5X4 streptococc
19	492.5	19.7	260	2	Q54971 streptococc
20	487.5	19.5	260	2	Q54739 streptococc
21	487.5	19.5	260	2	Q54738 streptococc
22	482	19.3	259	2	Q936G4 streptococc
23	444	17.8	233	2	Q8RR77 streptococc
24	444	17.8	258	16	Q85382 streptococc
25	434	17.4	258	2	Q9EZM3 streptococc
26	431	17.2	258	2	Q9ZNF2 streptococc
27	422	16.9	886	2	Q53481 porphyromon
28	303.5	12.1	136	16	Q99T49 streptococc
29	291.5	11.7	260	16	Q99T46 streptococc
30	291.5	11.7	261	2	Q9EZM8 streptococc
31	281.5	11.3	217	2	Q8RR75 streptococc
32	281.5	11.3	241	2	Q53585 streptococc
33	279.5	11.2	260	16	Q99S03 streptococc
34	272.5	10.9	108	2	Q9EZM5 streptococc
35	263	10.5	240	16	Q9F0L7 streptococc
36	262.5	10.5	258	16	Q9EZM4 streptococc
37	260.5	10.4	268	2	Q85217 streptococc
38	257.5	10.3	260	16	Q931M4 streptococc
39	237.5	9.5	239	16	Q99T47 streptococc
40	236.5	9.5	239	2	Q9EZM7 streptococc
41	231.5	9.3	256	2	Q8VLM7 streptococc
42	230.5	9.2	242	2	Q93CC6 streptococc
43	218	8.7	218	2	Q8RR75 streptococc
44	218	8.7	242	16	Q85383 streptococc
45	214	8.6	242	2	Q54476 streptococc

ALIGNMENTS

RESULT 1					
ID	Q9AJD2	PRELIMINARY;	PRT;	398 AA.	
AC	Q9AJD2;				
DT	01-JUN-2001 (T-REMBREL. 17, Created)				
DT	01-JUN-2001 (T-REMBREL. 17, Last sequence update)				
DT	01-OCT-2001 (T-REMBREL. 18, Last annotation update)				
DE	Pyrogenic exotoxin B.				
GN	SPE B.				
OS	Streptococcus pyogenes.				
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;				
OC	Streptococcaceae; Streptococcus.				
OX	NCBI_TaxID=1314;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	SRRAIN-NL31;				
RA	Matnabe Y., Ohkuni H.;				
RT	"Cloning and expression analysis of Streptococcal pyrogenic exotoxin B				
RT	(SPE-B)/Streptococcal cysteine protease (SCP)."				
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AB051298; BAB40954.1; -				
DR	InterPro; IPR000200; Peptidase_C10.				
DR	Pfam; PF01640; Peptidase_C10; 1.				
DR	PRINTS; PRO0797; STREPTOPAIN.				
DR	SEQUENCE 398 AA; 43218 MW; 07D1F534E7887CDD CRC64;				
SO					
Query Match	53.0%; Score 1324.5; DB 2; Length 398;				
Best Local Similarity	91.1%; Pred. No. 2.7e-76;				
Matches 257; Conservative	6; Mismatches 8; Indels 11; Gaps 5;				
QY	192 FTOSKYLMTIKDNETLSNOIEVYLT---KQPVKSLDSKGIHNOGNPNLTPVI 248				
DB	120 FMES-YEQIKENKILDT-----TYAGTAETKQPVKSLDSKGIHNOGNPNLTPVI 173				
QY	249 EKVPFGQSFVGQHAATGCVATAQAQIMKYHNPKNGLKYTYTLSSNNPFGNPKLFA 308				
DB	174 EKVPFGQSFVGQHAATGCVATAQAQIMKYHNPKNGLKYTYTLSSNNPFGNPKLFA 233				
QY	309 AISTROYMNWNLFTYGRGSSNVOKMAISELMADVGISVMDYGPSSGSGSSRVQRAK 368				

DB 234 AISTROYNNNNILPTYSGRESNVOKMAISELMADVGISVDMYDGPSSGSSGSRVORALK 293
 QY 369 ENFGYNSVHOINRSDFS-ODWEAQDKELSONOPYYYG-GKVGHAFTVIGADGRNFY 426
 DB 294 ENFGYNSVHOINRSDFSODKWSQIDKELSONOPYYYGKVGHAFTVIGADGRNFY 353
 QY 427 HVMGNGVSDGFEFRDLALNPALGTGGAGGFGNGQSAVVG 468
 DB 354 HVMGNGVSDGFEFRDLALNPALGTGGAGGFGNGQSAVVG 395

RESULT 2

093L02 PRELIMINARY: PRT: 344 AA.
 ID 093L02; PRELIMINARY: PRT: 344 AA.
 AC 093L02; PRELIMINARY: PRT: 344 AA.
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Cysteine protease SpeB (Fragment).
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 NCBI_Taxid=1314;
 RN [1]
 RP STRAIN-SP268;
 RC Jadaou J., Eyal O., Sela S.;
 RT "Role of car, hasa, and speB genes in the internalization of
 RT Streptococcus pyogenes by epithelial cells."
 RT Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AY035886; AAK71464.1;
 DR MEROPS: C10.001;
 DR InterPro: IPR000200; Peptidase_C10.
 DR Pfam: PF01640; Peptidase_C10; 1.
 DR KEGG: K01640; Peptidase_C10; 1.
 FT NON_TER 1 1
 FT NON_TER 344 344
 SQ SEQUENCE 344 AA: 37345 MW: F80A9BD05B541909 CRC64;

Query Match 51.7%; Score 1293.5; DB 2; Length 344;
 Best Local Similarity 91.3%; Pred. No. 2.1e-74;
 Matches 251; Conservative 5; Mismatches 8; Indels 11; Gaps 5;
 QY 192 FTQSKYLMYKNDNTLDSNVOIEYLT---KQPVKSLDSKGIHNGNPNYLLPVI 248
 DB 76 FMES-YVEQIKENKRLDT---TYAGTAELKQPVKSLDSKGIHNGNPNYLLPVI 129
 QY 249 EKVPGESEFYGQHAATGCAVATATQIMKYHNPNKGLKDYTYTLSSNNPFNHPKRLFA 308
 DB 130 EKVPGESEFYGQHAATGCAVATATQIMKYHNPNKGLKDYTYTLSSNNPFNHPKRLFA 189
 QY 309 AISTROYNNNNILPTYSGRESNVOKMAISELMADVGISVDMYDGPSSGSSGSRVORALK 368
 DB 190 AISTROYNNNNILPTYSGRESNVOKMAISELMADVGISVDMYDGPSSGSSGSRVORALK 249
 QY 369 ENFGYNSVHOINRSDFS-ODWEAQDKELSONOPYYYG-GKVGHAFTVIGADGRNFY 426
 DB 250 ENFGYNSVHOINRSDFSODKWSQIDKELSONOPYYYGKVGHAFTVIGADGRNFY 309
 QY 427 HVMGNGVSDGFEFRDLALNPALGTGGAGGFGNG 461
 DB 310 HVMGNGVSDGFEFRDLALNPALGTGGAGGFGNG 344

RESULT 3

054779 PRELIMINARY: PRT: 236 AA.
 ID 054779; PRELIMINARY: PRT: 236 AA.
 AC 054779; 054613; 054736; 054740; 054741;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Type A exotoxin precursor (Fragment).

GN SPEA.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 NCBI_Taxid=1314;
 RN [1]
 RP STRAIN-MGAS624 AND MGAS158 AND MGAS485 AND MGAS491, AND MGAS495;
 RC MEDLINE=92044323; PubMed=1940804;
 RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
 RT "Characterization and clonal distribution of four alleles of the speA
 RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
 RT Streptococcus pyogenes."
 RL J. Exp. Med. 174:1271-1274(1991).
 DR EMBL: X61569; CAA43767.1;
 DR EMBL: X61572; CAA43770.1;
 DR EMBL: X61578; CAA43766.1;
 DR EMBL: X61570; CAA43768.1;
 DR EMBL: X61571; CAA43769.1;
 DR HSSP: P08095; 1812.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph-Strep_toxin; 1.
 DR Pfam: PF02876; Staph-Strep_toxin_C; 1.
 DR PRINTS: PR00279; BACTRTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 22 POTENTIAL.
 FT CHAIN 23 >236 TYPE A EXOTOXIN.
 FT NON_TER 236 236
 SQ SEQUENCE 236 AA: 27468 MW: 29DF2AD575623A84 CRC64;

Query Match 43.9%; Score 1096.5; DB 2; Length 236;
 Best Local Similarity 98.6%; Pred. No. 3.9e-62;
 Matches 208; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 2 QQDPDSQLRRSSLYKNIQNYFLYEGDPYTHENKVSQQLRSHDLIYNSGNYRKLKT 61
 DB 23 QQDPDSQLRRSSLYKNIQNYFLYEGDPYTHENKVSQQLRSHDLIYNSGNYRKLKT 82
 QY 62 ELKQEMATLFEKKNIDIVGEVYHLCYLCEAERSACI-GVYTNREGNHLTPKRIYVK 120
 DB 83 ELKQEMATLFEKKNIDIVGEVYHLCYLCEAERSACI-GVYTNREGNHLTPKRIYVK 142
 QY 121 VSDIGIOSLSEFDLETNKKMTYAEIDYKRAKYLTDNKKOLYTNCPSPSYETGIKIPKNE 180
 DB 143 VSDIGIOSLSEFDLETNKKMTYAEIDYKRAKYLTDNKKOLYTNCPSPSYETGIKIPKNE 202
 QY 181 SFWFDFPEPEFTOSKYLMIYKNDNTLDSNT 211
 DB 203 SFWFDFPEPEFTOSKYLMIYKNDNTLDSNT 233

RESULT 4

09R931 PRELIMINARY: PRT: 222 AA.
 ID 09R931; PRELIMINARY: PRT: 222 AA.
 AC 09R931; PRELIMINARY: PRT: 222 AA.
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Exotoxin A (Fragment).
 GN SPEA.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 NCBI_Taxid=1314;
 RN [1]
 RP STRAIN-MGAS624 AND MGAS158 AND MGAS485 AND MGAS491, AND MGAS495;
 RC MEDLINE=92044323; PubMed=1940804;
 RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
 RT "Characterization and clonal distribution of four alleles of the speA
 RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
 RT Streptococcus pyogenes."
 RL J. Exp. Med. 174:1271-1274(1991).
 DR EMBL: X61569; CAA43767.1;
 DR EMBL: X61572; CAA43770.1;
 DR EMBL: X61578; CAA43766.1;
 DR EMBL: X61570; CAA43768.1;
 DR EMBL: X61571; CAA43769.1;
 DR HSSP: P08095; 1812.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph-Strep_toxin; 1.
 DR Pfam: PF02876; Staph-Strep_toxin_C; 1.
 DR PRINTS: PR00279; BACTRTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 22 POTENTIAL.
 FT CHAIN 23 >236 TYPE A EXOTOXIN.
 FT NON_TER 236 236
 SQ SEQUENCE 236 AA: 27468 MW: 29DF2AD575623A84 CRC64;

Genetic linkage of exotoxin alleles and emm gene markers for tissue tropism in group A streptococci.
RT J. Infect. Dis. 179:627-636(1999).
DR EMBL: AF055698; AAD1624.1; -
DR HSSP: P08095; 1B12.
DR InterPro: IPR001961; Strep/Strep-toxin.
DR Pfam: PF01123; Strep_Strep_toxin; 1.
DR Pfam: PF02876; Strep_Strep_toxin_C; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 1
FT NON_TER 222 222
SQ SEQUENCE 222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;

Query Match
Best Local Similarity 98.1%; Score 1095.5; DB 2; Length 222;
Matches 207; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 2 QODPPSQLRSSLVKLNQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLT 61
DB 11 QODPPSQLRSSLVKLNQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLT 70
OY 62 ELKNOEMATLFKKNVDIYGEYHLCYLCENASACI-GGYTNEGHNLEIPKKIYK 120
DB 71 ELKNOEMATLFKKNVDIYGEYHLCYLCENASACIYGGVTNEGHNLEIPKKIYK 130
OY 121 VSIDGIQSLSFDIETNKKMVTAAOELDYKVRKYLTDNKKOLYTNGPSKYETGYIKFIPKKE 180
DB 131 VSIDGIQSLSFDIETNKKMVTAAOELDYKVRKYLTDNKKOLYTNGPSKYETGYIKFIPKKE 190
OY 181 SFWFDFPEPEPTQSKYLMYKDNETLDSNT 211
DB 191 SFWFDFPEPEPTQSKYLMYKDNETLDSNT 221

RESULT 5
P97163 PRELIMINARY; PRT; 236 AA.
ID P97163
AC P97163; P97164;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156; AND MGAS500;
RX MEDLINE-92044323; PubMed-1940804;
RA Nelson K., Schlievert P.M., Seldner R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.";
RT J. Exp. Med. 174:1271-1274(1991).
RL EMBL: X61556; CAA43754.1; -
DR EMBL: X61557; CAA43755.1; -
DR EMBL: X61560; CAA43758.1; -
DR EMBL: X61555; CAA43753.1; -
DR EMBL: X61558; CAA43756.1; -
DR EMBL: X61559; CAA43757.1; -
DR EMBL: X61554; CAA43752.1; -
DR HSSP: P08095; 1B12.
DR InterPro: IPR001961; Strep/Strep-toxin.
DR Pfam: PF01123; Strep_Strep_toxin; 1.
DR Pfam: PF02876; Strep_Strep_toxin_C; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.

FT NON_TER 1 1
FT SIGNAL <1 22
FT CHAIN 23 >236
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27454 MW; 3FB3F41ABDC13A84 CRC64;

Query Match
Best Local Similarity 98.1%; Score 1095.5; DB 2; Length 236;
Matches 207; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 2 QODPPSQLRSSLVKLNQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLT 61
DB 23 QODPPSQLRSSLVKLNQNIYFLYEGDPVTHENVKSVQDLRSHDLIYNVSGPNYDKLT 82
OY 62 ELKNOEMATLFKKNVDIYGEYHLCYLCENASACI-GGYTNEGHNLEIPKKIYK 120
DB 83 ELKNOEMATLFKKNVDIYGEYHLCYLCENASACIYGGVTNEGHNLEIPKKIYK 142
OY 121 VSIDGIQSLSFDIETNKKMVTAAOELDYKVRKYLTDNKKOLYTNGPSKYETGYIKFIPKKE 180
DB 143 VSIDGIQSLSFDIETNKKMVTAAOELDYKVRKYLTDNKKOLYTNGPSKYETGYIKFIPKKE 202
OY 181 SFWFDFPEPEPTQSKYLMYKDNETLDSNT 211
DB 203 SFWFDFPEPEPTQSKYLMYKDNETLDSNT 233

RESULT 6
O57453 PRELIMINARY; PRT; 236 AA.
ID O57453
AC O57453;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS496;
RX MEDLINE-92044323; PubMed-1940804;
RA Nelson K., Schlievert P.M., Seldner R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.";
RT J. Exp. Med. 174:1271-1274(1991).
RL EMBL: X61562; CAA43760.1; -
DR EMBL: X61563; CAA43761.1; -
DR EMBL: X61567; CAA43765.1; -
DR EMBL: X61561; CAA43759.1; -
DR EMBL: X61564; CAA43762.1; -
DR EMBL: X61565; CAA43763.1; -
DR EMBL: X61566; CAA43764.1; -
DR HSSP: P08095; 1B12.
DR InterPro: IPR001961; Strep/Strep-toxin.
DR Pfam: PF01123; Strep_Strep_toxin; 1.
DR Pfam: PF02876; Strep_Strep_toxin_C; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22
FT CHAIN 23 >236
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27484 MW; 2EF7F41AAC53600 CRC64;

Query Match
Best Local Similarity 97.6%; Score 1089.5; DB 2; Length 236;
Matches 206; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

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QY 2 QQDPDPSSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVDOILSHDLIYVNSGPNYDKLKT 61
Db 23 QQDPDPSSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVDOILSHDLIYVNSGPNYDKLKT 82
QY 62 ELKQEMATLFFKDKNIDIVGEYHYHLCLYCENASRSACI-GGYVNRGNHLEIPKTIYVK 120
Db 83 ELKQEMATLFFKDKNIDIVGEYHYHLCLYCENASRSACIYGGVNHGEGNHLIEIPKTIYVK 142
QY 121 VSIDGIOSLSFDIETNKKMVTAGELDYKVRKYLTDNKOQLYTNGPSKYETGYIKFIPKKE 180
Db 143 VSIDGIOSLSFDIETNKKMVTAGELDYKVRKYLTDNKOQLYTNGPSKYETGYIKFIPKKE 202
QY 181 SFWFDFEPPEFTOSKYLMIYKDNETLDSNT 211
Db 203 SFWFDFEPPEFTOSKYLMIYKDNETLDSNT 233

RESULT 7
ID 054696 PRELIMINARY; PRT; 236 AA.
AC 054696;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156;
RX MEDLINE-92044323; PubMed-1940804;
RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL; X61573; CAA43771.1; -.
DR HSSP; P08095; 1812.
DR InterPro: IPR001961; Strep/Strep-toxin.
DR Pfam; PF01123; Strep-Strep-toxin; 1.
DR PRINTS; PR02876; Strep-Strep-toxin; 1.
DR PROSITE; PS00279; BACTRLOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236
SQ SEQUENCE 236 AA; 27575 MW; 70F54120E79127DF CRC64;

Query Match 39.58; Score 986.5; DB 2; Length 236;
Best Local Similarity 88.28; Pred. No. 3,7e-55;
Matches 186; Conservative 13; Mismatches 11; Indels 1; Gaps 1;
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Db 203 TFWDFEPPEFTOSKYLMIYKDNETLDSNT 233

RESULT 8
ID 09S524 PRELIMINARY; PRT; 222 AA.
AC 09S524;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Exotoxin type A (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-D633;
RX MEDLINE-99137798; PubMed-9952369;
RA Bessen D.E., Izzo M.W., Florentino T.R., Carling R.M.,
RA Hollingshead S.K., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci."
RL J. Infect. Dis. 179:627-636(1999).
DR EMBL; AF029051; AAD21315.1; -.
DR HSSP; P08095; 1812.
DR InterPro: IPR001961; Strep/Strep-toxin.
DR Pfam; PF01123; Strep-Strep-toxin.
DR PRINTS; PR02876; Strep-Strep-toxin; 1.
DR PROSITE; PS00279; BACTRLOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 222 AA; 25884 MW; 121F846099281878 CRC64;

Query Match 39.38; Score 981.5; DB 2; Length 222;
Best Local Similarity 87.78; Pred. No. 7.1e-55;
Matches 185; Conservative 13; Mismatches 12; Indels 1; Gaps 1;
```

```
QY 2 QQDPDPSSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVDOILSHDLIYVNSGPNYDKLKT 61
Db 11 QQDPDPSSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVDOILSHDLIYVNSGPNYDKLKT 70
QY 62 ELKQEMATLFFKDKNIDIVGEYHYHLCLYCENASRSACI-GGYVNRGNHLEIPKTIYVK 120
Db 71 ELKQEMATLFFKDKNIDIVGEYHYHLCLYCENASRSACIYGGVNHGEGNHLIEIPKTIYVK 130.
QY 121 VSIDGIOSLSFDIETNKKMVTAGELDYKVRKYLTDNKOQLYTNGPSKYETGYIKFIPKKE 180
Db 131 VSIDGIOSLSFDIETSKMVTAGELDYKVRKYLTDNKOQLYTNGPSKYETGYIKFIPKKE 190
QY 181 SFWFDFEPPEFTOSKYLMIYKDNETLDSNT 211
Db 191 TFWDFEPPEFTOSKYLMIYKDNETLDSNT 221

RESULT 9
ID 0938P4 PRELIMINARY; PRT; 222 AA.
AC 0938P4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Pyrogenic exotoxin A (Fragment).
GN SPEA.
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
```

RC STRAIN-4951;
 RA Kalia A., Bessen D.E.;
 RT "Presence of streptococcal pyrogenic exotoxin A and C genes in human
 RT isolates of group G streptococci";
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF049745; AAL06068.1;
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01133; Staph_strep_toxin; 1.
 DR Pfam: PF02876; Staph_strep_toxin; 1.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 222
 SQ SEQUENCE 222 AA; 25884 MW; 121F846092818F8 CRC64;

Query Match 39.3%; Score 981.5; DB 2; Length 222;
 Best Local Similarity 87.7%; Pred. No. 7.1e-55;
 Matches 185; Conservative 13; Mismatches 12; Indels 1; Gaps 1;

QY 2 QODPDSQIHRSSLVKNIQNIYFLYEGDPYTHENKSVQDLRSHDLIYNVSGPNYDKLTK 61
 DB 11 QODPNPQIHRSSLVKNIQNIYFLYEGDPYTHENKSVQDLRSHDLIYNVSGPNYDKLTK 70
 QY 62 ELKNQEMATLFRKNDIYGEVYHLCYLCENAKRSACTGGVYTNREGNLEIPKTIYVK 120
 DB 71 ELKNREKSTLEKKNNDIYGEVYHLCYLCENAKRRACIYGVYTNREGNLEIPKTIYVK 130
 QY 121 VSIDGQSLSFDEITNKKKVTAGQELQYKRYLNDKQLYTNKPSKYEYIKFIPRKE 180
 DB 131 VSIDGQSLSFDEITNKKKVTAGQELQYKRYLNDKQLYTNKPSKYEYIKFIPRKE 190
 QY 181 SFWFDFEPEPEFTQSKYLMYKDNETLDSNT 211
 DB 191 TFWDFEPEPEFTQSKYLMYKDNETLDSNT 221

RESULT 10
 ID 053678 PRELIMINARY; PRT; 239 AA.
 AC 053678;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Enterotoxin (Fragment).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Staphylococcus.
 OC NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94011313; PubMed=8406814;
 RA Mart J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 RT biological and evolutionary implications";
 RL Infect. Immun. 61:4254-4262(1993).
 DR EMBL; L13376; AAA26620.1;
 DR HSSP; P34071; ISE2.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01133; Staph_strep_toxin; 1.
 DR Pfam: PF02876; Staph_strep_toxin; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1
 FT NON_TER 222
 SQ SEQUENCE 239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;

Query Match 20.6%; Score 516; DB 2; Length 239;
 Best Local Similarity 45.1%; Pred. No. 2.7e-25;
 Matches 106; Conservative 44; Mismatches 69; Indels 16; Gaps 6;
 QY 2 QODPDSQIHRSSLVKNIQNIYFLYEGDPYTHENKSVQDLRSHDLIYNVSG---PNYD 57
 DB 3 QDPPTDELHKASKFTGLMKNKVLVYDDRYVSATKVSVDKFLAHLIYNISDKKLKND 62

QY 58 KLTTELKNOEMATLFRKNDIYGEVYHLCYLC-----NAERSACTIGVTNREGN 110
 DB 63 KVTTELLMEDLAKKYDEVDVGSNTYVNCSSKDNKGVTKGKTCMGTGTRKEGN 122
 QY 111 LEIPK-KIYKVSIDGQSLSFDEITNKKKVTAGQELQYKRYLNDKQLYTNKPSKYE 168
 DB 123 FDMGKLQNVLIIRYENKRNITSEVQDKRSVTAQELDIARFLINKRLYEFNSPYE 182
 QY 169 TGYIKFIPKKSSEFWDFEPEP--EFTQSKYLMYKDNETLDS-NTQIEVYLTTK 220
 DB 183 TGYIKFIEENNNTFWDMPAPDQKFDQSKYLMYKDNKTVDSKSVKIEVHLTK 237

RESULT 11
 QY 09F0L6 PRELIMINARY; PRT; 271 AA.
 ID 09F0L6;
 AC 09F0L6;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Staphylococcal enterotoxin C-bovine.
 GN SEC-BOV.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Staphylococcus.
 OC NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2056668; PubMed=11114901;
 RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
 RA Meaney W.J., Smyth C.J.;
 RT "Characterization of a putative pathogenicity island from bovine
 RT Staphylococcus aureus encoding multiple superantigens";
 RL J. Bacteriol. 183:63-70(2001).
 DR EMBL; AF217235; AAG29599.1;
 DR HSSP; P34071; ISE2.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01133; Staph_strep_toxin.
 DR Pfam: PF02876; Staph_strep_toxin; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 SQ SEQUENCE 271 AA; 31267 MW; 3493F6228B042F10 CRC64;

Query Match 20.6%; Score 516; DB 2; Length 271;
 Best Local Similarity 45.1%; Pred. No. 3.2e-25;
 Matches 106; Conservative 44; Mismatches 69; Indels 16; Gaps 6;

QY 2 QODPDSQIHRSSLVKNIQNIYFLYEGDPYTHENKSVQDLRSHDLIYNVSG---PNYD 57
 DB 35 QDPPTDELHKASKFTGLMKNKVLVYDDRYVSATKVSVDKFLAHLIYNISDKKLKND 94
 QY 58 KLTTELKNOEMATLFRKNDIYGEVYHLCYLC-----NAERSACTIGVTNREGN 110
 DB 95 KVTTELLMEDLAKKYDEVDVGSNTYVNCSSKDNKGVTKGKTCMGTGTRKEGN 154
 QY 111 LEIPK-KIYKVSIDGQSLSFDEITNKKKVTAGQELQYKRYLNDKQLYTNKPSKYE 168
 DB 155 FDMGKLQNVLIIRYENKRNITSEVQDKRSVTAQELDIARFLINKRLYEFNSPYE 214
 QY 169 TGYIKFIPKKSSEFWDFEPEP--EFTQSKYLMYKDNETLDS-NTQIEVYLTTK 220
 DB 215 TGYIKFIEENNNTFWDMPAPDQKFDQSKYLMYKDNKTVDSKSVKIEVHLTK 269

RESULT 12
 ID 006532 PRELIMINARY; PRT; 239 AA.
 AC 006532;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

[illegible]

RESULT 15

ID	006531;	PRELIMINARY;	PRT;	239 AA.
AC	006531;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Enterotoxin type C-4 (SCC4446) (fragment).			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;			
CC	Staphylococcus.			
ON	NCBI_TaxID=1280;			
RX	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=446;			
RX	MEDLINE=94011313; PubMed=8406814;			
RA	Marr J.C., Lyon J.D., Roberson J.R., Lapher M., Bohach G.A.;			
RT	Characterization of novel type C staphylococcal enterotoxins:			
RL	biological and evolutionary implications.			
FT	Infect. Immun. 61:4254-4262(1993).			
CC	-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION			
CC	STAPHYLOCOCCAL FOOD POISONING SYNDROME.			
CC	-1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES			
CC	PYROGENIC EXOTOXINS ARE ALL RELATED.			
DR	EMBL: L13374; AAA26618.1; -			
DR	HSSP: P34071; 1SE2.			
DR	InterPro: IPR001961; Stap_Strep_toxin.			
DR	Pfam: PF01123; Stap_Strep_toxin; 1.			
DR	Pfam: PF02876; Stap_Strep_tox.C; 1.			
DR	PRINTS: PR00279; BACTRLTOXIN.			
DR	PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.			
DR	PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.			
FT	Enterotoxin; Toxin; Superantigen.			
FT	NON_TER			
SO	SEQUENCE			
	239 AA; 27612 MW; BB7BD6204731ED24 CRC64;			

Search completed: June 23, 2003, 16:14:55
Job time : 70.2976 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 16:06:40 ; Search time 18.2253 seconds

(without alignments)
1065.053 Million cell updates/sec

Title: US-10-002-784A-27

Perfect score: 2500

Sequence: 1 MQQDPSPSQHRSSIVKNIQ.....ALGTGGAGGFGNGYQSAVVG 468

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SWISSProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1327.5	53.1	398	1	SPEB_STRPY
2	1129	45.2	251	1	SPEA_STRPY
3	541	21.6	266	1	ETXB_STAU
4	513	20.5	266	1	ETC3_STAM
5	510	20.4	266	1	ETC2_STAU
6	509	20.4	266	1	ETC1_STAU
7	444	17.8	258	1	ETXG_STAM
8	422	16.9	868	1	PRTP_PORGI
9	295.5	11.8	258	1	ETXD_STAU
10	257.5	10.3	257	1	ETXA_STAM
11	256.5	10.3	257	1	ETXE_STAU
12	203.5	8.1	236	1	SPEH_STRPY
13	183	7.3	235	1	SPEG_STRPY
14	152	6.1	234	1	SPEG_STRPY
15	123	4.9	1147	1	CGA2_HELPY
16	119.5	4.8	1182	1	CGA1_HELPY
17	117	4.7	1186	1	CGA_HELPY
18	116.5	4.7	894	1	DSCL_HUMAN
19	115.5	4.6	908	1	DPOL_BORBU
20	115.5	4.6	1444	1	RRPL_RDVA
21	114.5	4.6	624	1	VE70_METUA
22	114.5	4.6	3135	1	S230_PIARO
23	114	4.6	964	1	DPOL_CHEPV
24	113.5	4.5	1221	1	V143_NPVAC
25	111.5	4.5	476	1	RP3_SACBA
26	110.5	4.4	554	1	V478_RICPR
27	110.5	4.4	762	1	MUS2_HELPJ
28	110.5	4.4	1386	1	RPOD_MARPO
29	110	4.4	817	1	RPOD_ASTIO
30	109	4.4	762	1	MUS2_HELPY
31	108.5	4.3	469	1	PPAS_KLUOTA
32	108.5	4.3	617	1	V237_BUCAI
33	108	4.3	735	1	CIGB_DICDI

34	107.5	4.3	319	1	TH80_YEAST
35	107.5	4.3	2136	1	YCF2_MARPO
36	107	4.3	643	1	K2C1_HUMAN
37	106.5	4.3	623	1	PPID_BUCAI
38	106.5	4.3	716	1	PBPB_BACSU
39	106.5	4.3	838	1	YRAU_ECOLI
40	106.5	4.3	2710	1	TOXA_CLODI
41	106	4.2	794	1	2148_MOUSE
42	105.5	4.2	592	1	RB50_HUMAN
43	105.5	4.2	766	1	DPp4_HUMAN
44	105	4.2	446	1	NAOX_ENTFA
45	105	4.2	543	1	APPA_BACSU

ALIGNMENTS

RESULT 1

ID	SPEB_STRPY	STANDARD	PRT:	398 AA.
AC	P00788; P26296; Q54960; Q54961; Q54962; Q54963; Q54964; Q54965; Q54966; Q54967; Q54968; Q57024; Q57082; Q57202; Q57211; Q57212;			
AC	Q95680;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Streptopain precursor (EC 3.4.22.10) (Streptococcal cysteine proteinase)			
DE	Streptococcus (Streptococcus peptidase A) (SPF) (Exotoxin type B) (SPE B).			
GN:	SPEB OR SPY2039 OR SPYM18-2099.			
OS	Streptococcus pyogenes, and			
OS	Streptococcus pyogenes (serotype M18).			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
OX	NCBI_TaxID=1314, 186103;			
LN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 28-32 AND 146-162.			
RC	STRAIN=86-858, and NY-5;			
RX	MEDLINE=90330563; PubMed=2198264;			
RA	Hauser A.R., Schlievert P.M.,			
RT	gene and relationship of the streptococcal pyrogenic exotoxin type B			
RT	proteinase precursor.";			
RL	J. Bacteriol. 172:4536-4542(1990).			
LN	[2]			
RP	SEQUENCE FROM N.A., AND CHARACTERIZATION.			
RC	STRAIN=Various MGAS strains;			
RX	MEDLINE=94285789; PubMed=7516997;			
RA	Kaplan V., Topouzis S., Majesky M.W., Li L.L., Hamrick M.R.,			
RA	Hanill R.J., Patti J.M., Musser J.M.;			
RT	A conserved Streptococcus pyogenes extracellular cysteine protease			
RT	cleaves human fibronectin and degrades vitronectin.";			
RL	Microb. Pathog. 15:327-346(1993).			
LN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=A-20 / Serotype M1.T1;			
RA	MU J.-J.;			
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.			
LN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SV / Serotype M23;			
RA	Hong K.;			
RT	"A novel cloning method used arbitrarily primed PCR.";			
RT	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.			
LN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SF370 / ATCC 700294 / Serotype M1;			
RX	MEDLINE=21192684; PubMed=11296296;			
RA	Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,			
RA	Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,			
RA	Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,			
RA	Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;			
RT	"Complete genome sequence of an M1 strain of Streptococcus			

RT pyogenes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MGAS8232 / Serotype M18;
 RX MEDLINE-21927593; PubMed-11917108;
 RA Smoot J.C., Barblan K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
 RA Sylva G.L., Studevant D.E., Ricklefs S.M., Porcella S.F.,
 RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
 RA Kapur V., Daly J.A., Vessy L.G., Musser J.M.;
 RT "Genome sequence and comparative microarray analysis of serotype M18
 RT group A Streptococcus strains associated with acute rheumatic fever
 RT outbreaks";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
 RN [7]
 RP PRELIMINARY SEQUENCE OF 28-86 AND 121-398.
 RA Yonaha K., Elliott S.D., Liu T.-Y.,
 RT "Primary structure of zymogen of streptococcal proteinase.";
 RL J. Protein Chem. 1:317-334(1982).
 RN [8]
 RP PRELIMINARY SEQUENCE OF 146-398.
 RX MEDLINE-76190087; PubMed-1270417;
 RA Tai J.Y., Kortt A.A., Liu T.-Y., Elliott S.D.;
 RT "Primary structure of streptococcal proteinase. III. Isolation of
 RT cyanogen bromide peptides: complete covalent structure of the
 RT polypeptide chain.";
 RL J. Biol. Chem. 251:1955-1959(1976).
 RN [9]
 RP FUNCTION.
 RC STRAIN-NZ131 / Serotype M49.T14;
 RX MEDLINE-99081733; PubMed-9864206;
 RA Kuo C.-F., Wu J.-J., Tsai P.-J., Kao F.-J., Lei H.-Y., Lin M.T.,
 RA Lin Y.-S.;
 RT "Streptococcal pyrogenic exotoxin B induces apoptosis and reduces
 RT phagocytic activity in U937 cells.";
 RL Infect. Immun. 67:126-130(1999).
 RN [10]
 RP FUNCTION.
 RC STRAIN-A-20 / Serotype M1.T1;
 RX MEDLINE-99386817; PubMed-10456871;
 RA Tsai P.-J., Lin Y.-S., Kuo C.-F., Lei H.-Y., Wu J.-J.;
 RT "Group A Streptococcus induces apoptosis in human epithelial cells.";
 RL Infect. Immun. 67:4334-4339(1999).
 CC -1- FUNCTION: IMPORTANT STREPTOCOCCAL VIRULENCE FACTOR WHICH CLEAVES
 CC HUMAN FIBRONECTIN AND DEGRADES VITRONECTIN. ALSO CLEAVES HUMAN
 CC IL1B PRECURSOR TO FORM BIOLOGICALLY ACTIVE IL1B. CAN INDUCE
 CC APOPTOSIS IN HUMAN MONOCYTES AND EPITHELIAL CELLS IN VITRO. AND
 CC REDUCES PHAGOCYTIC ACTIVITY IN MONOCYTIC CELLS. THUS, MAY PLAY A
 CC ROLE IN BACTERIAL COLONIZATION, INVASION, AND INHIBITION OF WOUND
 CC HEALING.
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage with hydrophobic
 CC residues at P2, P1 and P1'.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
 CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
 CC FEVER. HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
 CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
 CC FEVER.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C10.
 CC -----
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 CC -----
 CC EMBL; M86905; AAA26978.1; -
 CC EMBL; L26125; AAA26979.1; -
 CC EMBL; L26126; AAA26992.1; -
 CC EMBL; L26127; AAA26993.1; -
 CC EMBL; L26128; AAA26994.1; -

DR EMBL; L26130; AAA26996.1; -
 DR EMBL; L26131; AAA26997.1; -
 DR EMBL; L26132; AAA26998.1; -
 DR EMBL; L26133; AAA26999.1; -
 DR EMBL; L26134; AAA27000.1; -
 DR EMBL; L26135; AAA27001.1; -
 DR EMBL; L26136; AAA27002.1; -
 DR EMBL; L26137; AAA27003.1; -
 DR EMBL; L26138; AAA27004.1; -
 DR EMBL; L26139; AAA27005.1; -
 DR EMBL; L26140; AAA27006.1; -
 DR EMBL; L26141; AAA27007.1; -
 DR EMBL; L26142; AAA27008.1; -
 DR EMBL; L26143; AAA27009.1; -
 DR EMBL; L26144; AAA27010.1; -
 DR EMBL; L26145; AAA27011.1; -
 DR EMBL; L26146; AAA27012.1; -
 DR EMBL; L26147; AAA27013.1; -
 DR EMBL; L26148; AAA27014.1; -
 DR EMBL; L26149; AAA27015.1; -
 DR EMBL; L26150; AAA27016.1; -
 DR EMBL; L26151; AAA26980.1; -
 DR EMBL; L26152; AAA26981.1; -
 DR EMBL; L26153; AAA26982.1; -
 DR EMBL; L26154; AAA26983.1; -
 DR EMBL; L26155; AAA26984.1; -
 DR EMBL; L26156; AAA26985.1; -
 DR EMBL; L26157; AAA26986.1; -
 DR EMBL; L26158; AAA26987.1; -
 DR EMBL; L26159; AAA26988.1; -
 DR EMBL; L26160; AAA26989.1; -
 DR EMBL; L26161; AAA26990.1; -
 DR EMBL; L26162; AAA26991.1; -
 DR EMBL; AF104940; AAD17930.1; -
 DR EMBL; AB030578; BAB16027.1; -
 DR EMBL; AE006625; AAK34706.1; -
 DR EMBL; AE010112; AAL98559.1; -
 DR EMBL; L26129; AAA26995.1; -
 DR PIR; A37768; A37768.
 DR PIR; A00978; BPSOP.
 DR MEROPS; C10.001; -
 DR InterPro; IPR000200; Peptidase_C10.
 DR Pfam; PF01640; Peptidase_C10; 1.
 DR PRINTS; PRO0797; STREPTOPAIN.
 KW Hydrolyase; Thiol protease; Zymogen; Toxin; Signal; Complete proteome.
 FT SIGNAL 1 27
 FT PROPEP 28 145
 FT CHAIN 146 398
 FT ACT_SITE 192 192
 FT ACT_SITE 340 340
 FT VARIANT 8 8
 FT VARIANT 17 17
 FT VARIANT 80 80
 FT VARIANT 111 111
 FT VARIANT 137 137
 FT VARIANT 154 154
 FT VARIANT 193 193
 FT VARIANT 211 211
 FT VARIANT 293 293
 FT VARIANT 305 305
 FT VARIANT 308 308
 FT VARIANT 317 317
 FT VARIANT 384 384
 FT VARIANT 394 394
 FT CONFLICT 84 85
 FT CONFLICT 169 169
 FT CONFLICT 187 191
 I -> V (IN STRAIN SF370 AND A-20).
 G -> S (IN STRAIN MGAS 1896).
 V -> I (IN STRAIN MGAS 168).
 A -> V (IN STRAIN MGAS 165, 168, 429, 659, 660, 796, 800, 1719, 1838, 1882, 2017 AND 2018).
 T -> I (IN STRAIN MGAS 650).
 D -> N (IN STRAIN MGAS 684).
 V -> L (IN STRAIN A-20).
 L -> V (IN STRAINS MGAS 366, 427, 758, 1294, 1911, 1914A AND 1991).
 K -> R (IN STRAIN MGAS 587).
 I -> V (IN STRAIN MGAS 1901 AND SV).
 S -> G (IN STRAINS A-20, SF370, MGAS 429, 659, 807, 1226, 1719, 1832, 1842, 1871, 1872, 2017 AND 2018).
 A -> S (IN STRAINS MGAS 165, 168, 289, 302, 587, 1233 AND 1898).
 G -> D (IN STRAIN MGAS 1871).
 V -> I (IN STRAIN MGAS 366 AND 1294).
 ST -> AS (IN REF. 7).
 L -> I (IN REF. 7).
 HAATG -> AATGH (IN REF. 7 AND 8).

Query Match 53.1%; Score 1327.5; DB 1; Length 398;
 Best Local Similarity 91.5%; Pred. No. 3.9e-80;
 Matches 258; Conservative 5; Mismatches 6; Indels 11; Gaps 5;

192 PTQSKYLMYKDNFTLDSNTQIEVYLT*--KQPVKSLDLSKGIHYNGNPNLLTPYI 248
 120 FMES-YVGEIKENKTKLDT-----TYAGTAEIKQPVKSLDLSKGIHYNGNPNLLTPYI 173
 249 ENKRGESQFVQGHATGCVATATQIMKRYHNPKNGLKDYTYTSSNNPNYHNPKNLFA 308
 174 EKVKPGESQFVQGHATGCVATATQIMKRYHNPKNGLKDYTYTSSNNPNYHNPKNLFA 233
 309 AISTQYNNMNLTPYSGRESNVQKMAISELMADYGISVDMYGPSSGAGSSRQORALK 368
 234 AISTQYNNMNLTPYSGRESNVQKMAISELMADYGISVDMYGPSSGAGSSRQORALK 293
 369 ENKRGESQFVQGHATGCVATATQIMKRYHNPKNGLKDYTYTSSNNPNYHNPKNLFA 426
 294 ENKRGESQFVQGHATGCVATATQIMKRYHNPKNGLKDYTYTSSNNPNYHNPKNLFA 353
 427 HYNMGVGVSDGFFRLDALNPALGTGGAGGPNYQSAVVG 468
 354 HYNMGVGVSDGFFRLDALNPALGTGGAGGPNYQSAVVG 395

RESULT 2

SPEA_STRPY STANDARD; PRT: 251 AA.

ID SPEA_STRPY

AC P08095;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin) (Spe A).

GN SPEA OR SPY18_0393.

OS Streptococcus pyogenes, and

OS Streptococcus pyogenes (serotype M18).

OC Bacteria: Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

NCBI_TaxID=1314, 186103;

NCBI_TaxID=1314, 186103;

SEQUENCE FROM N.A.

RE MEDLINE-86166804; Pubmed-3514452;

RA Weeks C.R., Ferretti J.J.;

*Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage

RT t12.*;

RL Infect. Immun. 52:144-150(1986).

RP SEQUENCE FROM N.A.

RE MEDLINE-86284313; Pubmed-3526093;

RA Johnson L.P., V'Fallen J.J., Schlievert P.M.;

*Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is

RT related to Staphylococcus aureus enterotoxin B.*;

RL Mol. Genet. 203:354-356(1986).

RP SEQUENCE FROM N.A.

RE STRAIN-MGAS823 / Serotype M18;

RC MEDLINE-21927593; Pubmed-11917108;

RA Smoot J.C., Barblan K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,

RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,

RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,

RA Kapur V., Daly J.A., Yeasty L.G., Musser J.M.;

*Genome sequence and comparative microarray analysis of serotype M18

RT group A Streptococcus strains associated with acute rheumatic fever

RL outbreaks.*;

RP Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).

RA X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).

RE MEDLINE-99094887; Pubmed-9878045;

RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,

O'Brien S.M., Tranter H.S., Acharya K.R.;

RT "Structural basis for the recognition of superantigen streptococcal
 RT pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell
 RT receptors." J. Biol. Chem. 268:18921-18928(1993).

RL EMBO J. 18:9-21(1999).

CC -1- SUBUNIT: Binds to major histocompatibility complex class II beta

CC chain.

CC -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE

CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET

CC FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE

CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC

CC FEVER.

CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.

CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN

CC FAMILY.

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CC

DR EMBL: U40453; AAC4868.1; -

DR EMBL: X03929; CAA27568.1; -

DR PIR: A26152; A26152.

DR PIR: S29659; S29659.

DR PIR: I812; 24-NOV-99.

DR InterPro: IPR01961; Strep/Strep-toxin.

DR Pfam: PF01123; Strep-Strep-toxin; 1.

DR Pfam: PF02876; Strep-Strep-toxin; 1.

DR PRINTS: PRO0279; BACTRTOXIN.

DR PROSITE: PS00277; STAPH-STREP-TOXIN_1; 1.

DR PROSITE: PS00278; STAPH-STREP-TOXIN_2; 1.

DR Toxin; Signal; 3D-structure.

KW SIGNAL; 1 30

FT CHAIN 1 31 251

FT DISULFID 117 128

FT CONFLICT 6 6

FT CONFLICT 17 18

FT CONFLICT 25 35

FT CONFLICT 40 40

FT CONFLICT 43 43

FT CONFLICT 47 59

FT CONFLICT 129 129

FT CONFLICT 165 178

FT CONFLICT 165 178

SO SEQUENCE 251 AA; 29246 MW; 54001PF4CCBFC3 CRC64;

Query Match 45.2%; Score 1129; DB 1; Length 251;

Best Local Similarity 97.7%; Pred. No. 2.2e-67;

Matches 216; Conservative 1; Mismatches 2; Indels 2; Gaps 2;

2 OODPDSQHRSSVNLONIFLYEGDVTENKVSQVQLSHDLIYVNSGPNYDKLT 61

DB 31 QODPDSQHRSSVNLONIFLYEGDVTENKVSQVQLSHDLIYVNSGPNYDKLT 90

62 ELKQEMATLFDKRNIDIVGEYHLCYLCENASACI-GGVNREGNHLIPKRIYK 120

DB 91 ELKQEMATLFDKRNIDIVGEYHLCYLCENASACIYGVNREGNHLIPKRIYK 150

121 VSDIGQSISFDLETNKKVTAQOELDYKRYKLTDKKOLYTNQSPKSYNGYKFIKPKKE 180

DB 151 VSDIGQSISFDLETNKKVTAQOELDYKRYKLTDKKOLYTNQSPKSYNGYKFIKPKKE 210

181 SFWFDFPPEPFTOSKYLMIYKDNFTLDSNT-OIEVYLTTK 220

DB 211 SFWFDFPPEPFTOSKYLMIYKDNFTLDSNT-OIEVYLTTK 251

RESULT 3

ETXB_STAAU STANDARD: PRT: 266 AA.
 ID ETXB_STAAU PRT: 266 AA.
 AC P01552;
 DT 21-JUN-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 13-JUN-2002 (Rel. 41, Last annotation update)
 DE Enterotoxin type B precursor (SEB).
 GN EMTB.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86168029; PubMed=3957869;
 RA Jones C.L., Khan S.A.;
 RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus."
 RL J. Bacteriol. 166:29-33(1986).
 RP SEQUENCE OF 40-91 FROM N.A.
 RA MEDLINE=85298255; PubMed=3898073;
 RA Raneill D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
 RT "Molecular cloning of staphylococcal enterotoxin B gene in Escherichia coli and Staphylococcus aureus."
 RL Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
 RP SEQUENCE OF 28-266 (S-6).
 RA MEDLINE=71007902; PubMed=5470821;
 RA Huang I.-Y., Bergdoll M.S.;
 RT "The primary structure of staphylococcal enterotoxin B. 3. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence."
 RL J. Biol. Chem. 245:3518-3525(1970).
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RA MEDLINE=93063291; PubMed=1436058;
 RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
 RT "Crystal structure of staphylococcal enterotoxin B, a superantigen."
 RL Nature 359:801-806(1992).
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
 RA MEDLINE=7203282; PubMed=8152483;
 RA Janderzky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G., Chl Y.I., Stuttfacher C., Strominger J.L., Wiley D.C.;
 RT "Three-dimensional structure of a human class II histocompatibility molecule complexed with superantigen."
 RL Nature 368:711-718(1994).
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
 RA MEDLINE=99096298; PubMed=9881971;
 RA Li H., Llera A., Tsuchiya D., Leder L., Yseern X., Schlievert P.M., Karjalainen K., Mariuzza R.A.;
 RT "Three-dimensional structure of the complex between a T cell receptor beta chain and the superantigen staphylococcal enterotoxin B."
 RL Immunity 9:807-816(1998).
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RA MEDLINE=98181012; PubMed=9514739;
 RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;
 RT "Crystal structure of microbial superantigen staphylococcal enterotoxin B at 1.5-A resolution: implications for superantigen recognition by MHC class II molecules and T-cell receptors."
 RL J. Mol. Biol. 277:61-79(1998).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN FAMILY.
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 CC -----
 DR EMBL: M1118; AAA8550.1; -
 DR PIR: A01815; ENSAB6.
 DR PIR: S27360; S27360.
 DR PDB: 1SEB; 20-JUN-96.
 DR PDB: 2SEB; 28-JAN-98.
 DR PDB: 3SEB; 27-MAY-98.
 DR PDB: 1SE3; 16-JUN-97.
 DR PDB: 1SE4; 15-OCT-97.
 DR PDB: 1SBB; 04-MAR-99.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01122; Staph_Strep_toxin.
 DR Pfam: PF02876; Staph_Strep_toxin; 1.
 DR PRINTS: PR00279; BACTRTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
 FT SIGNAL 1 27
 FT CHAIN 28 266
 FT DISULFID 120 140
 FT CONFLICT 56 58 DDN -> NND (IN REF. 3).
 FT CONFLICT 69 77 DOFLFDLI -> NEFDLYLI (IN REF. 3).
 FT CONFLICT 118 118 MISSING (IN REF. 3).
 FT CONFLICT 128 130 DIN -> NID (IN REF. 3).
 FT CONFLICT 133 135 QTD -> ENT (IN REF. 3).
 FT CONFLICT 149 150 NG -> GN (IN REF. 3).
 FT CONFLICT 156 156 Y -> YY (IN REF. 3).
 FT CONFLICT 185 186 OE -> EQ (IN REF. 3).
 FT CONFLICT 233 233 D -> N (IN REF. 3).
 FT CONFLICT 246 247 DN -> ND (IN REF. 3).
 SQ SEQUENCE 266 AA; 31436 MW; 86D417F61CF01B80 CRC64;
 Query Match 21.6%; Score 541; DB 1; Length 266;
 Best Local Similarity 47.7%; Pred. No. 9,4e-29;
 Matches 113; Conservative 39; Mismatches 67; Indels 18; Gaps 7;
 QY 2 QOQDPDSQLRRSSLSVKKL-QNIFYLRGDPVTHENKASVQULASHDLTVNSG--NYD 57
 DB 30 QPDKPDELHKSSFTGLMKNMVKLYDDNHSAINVSSIDQFLFDLYISIKTKTKLMDY 89
 QY 58 KLTELKNQMATLTKDNIDIVGEYYHYCYLCENA-----ERSACI-GGYVNR 107
 DB 90 NVNVEFNKKLADKKNKYVDVCANTYCYFSKTKNDNSQTKRCKMGGVTEHN 149
 QY 108 GNHLELPKTIKIVKVSIDIOSLSFDIETNKKVTAQELDYKVRKYLTNKKQLYTNGPSKY 167
 DB 150 GNLDKRYRSITVVEFDGKNILSFQVTKNKKYTAQELDYLRHLYLVKNNKLYEFNNSPY 209
 QY 168 EFGYIKFIPKKNKSFMPDFPREP--EFTQSKYLMYIKNDNTLDS-NTQIEVYLTQQ 221
 DB 210 EFGYIKFT-ENNSFWMDMPAPGDKFQDSKYLIMYNDNKMVDSKVKEVLYLTTRK 265
 RESULT 4
 ETXC_STAAU STANDARD: PRT: 266 AA.
 ID ETXC_STAAU PRT: 266 AA.
 AC P23313;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Enterotoxin type C-3 precursor (SEC3).
 GN EMTC3 OR SAN2009 OR SA1817.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
 OS Staphylococcus aureus (strain N315), and
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878, 158879, 1280;
 RN SEQUENCE FROM N.A.
 RP STRAIN-Mu50 / ATCC 700699, and N315;

[illegible]

```

FT      METAL      149      149      ZINC
SQ      SEQUENCE   266 AA: 30604 MW: 8407E18536FAC08 CRC64:

Query Match          20.4%: Score 510; DB 1; Length 266;
Best Local Similarity 44.3%; Pred. No. 1e-26;
Matches 104; Conservative 45; Mismatches 70; Indels 16; Gaps 6;

OY      2     GODPEPSLOHSS-LVKNLQNIIFYESDPTTHENVKSVDDLRSHDLIYNYSG---PRYD 57
DB      30     OPDPRLDELHHSSSEFTGTGMGNKKLYLDHYVSATIKVMXDKFLAHLDIYNSIDKRLKNYD 89
OY      58     KLKTELAKNOEMATLEFKDNINIDYGEVEYLCLCE-----NAERSACIGVTNRREGNH 110
DB      90     KYKTELLMEDLAKKRYKDEVDYGSNNYYVNCVFSSKDVGAVGYTGKTOMGGITRKHEBNH 149
OY      111    LEIP--KRIIVKVSIDGIQSISFDIEDTKKNAVTAOELDYKYRKYLTQNKOLYTNGPSKYE 168
DB      150    FDNGLNQVLIRVYENKRNTISFEVOTDRKSVAFOELDIAKANFLINKNKNIYEFNSSPYE 209
OY      169    TGYIFIKFNKSESFWDFPPBP--EFTOSKLIMIKNDNETLS-NTOIEVYLTRK 220
DB      210    TGyIKFIENNNGTETWYDMAPRGDKFDQSKILMINDMKIVDSVKILEVHLTRK 264

RESULT 6
ETC1_STAAU
ID      ETC1_STAAU      STANDARD:      PRF: 266 AA.
AC      P01553:
DT      21-JUL-1986 (Rel. 01, Created)
DT      01-JAN-1990 (Rel. 13, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Enterotoxin type C-1 precursor (SEC1).
GN      ENT1.
OS      Staphylococcus aureus.
OC      Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
OX      NCBI_Taxid=1280;
RN      [1]
RX      MEDLINE=88038352; PubMed=2823067;
RA      Bonach G.A., Schlievert P.M.;
RT      "Nucleotide sequence of the staphylococcal enterotoxin CI gene and
RL      relatedness to other pyrogenic toxins.";
RM      Mol. Gen. Genet. 209:15-20(1987).
RN      [2]
RP      SEQUENCE OF 28-266.
RX      MEDLINE=83213327; PubMed=6189824;
RA      Schmidt J.J., Spero L.;
RT      "The complete amino acid sequence of staphylococcal enterotoxin CI.";
RL      J. Biol. Chem. 258:6300-6306(1983).
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC      STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC      -1 SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC      FAMILY.
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-----
DR      EMBL, X05815; CA29260.1; .
DR      PIR, A01816; ENSAC1.
DR      HSP, P34071; 1SR2.
DR      InterPro: IPR001961; Staph/Strep_toxin.
DR      Pfam: PF081123; Staph_Strep_toxin_1.
DR      pfam, PF02876; Staph_Strep_tox_C; 1.
DR      PRINTS: PR00279; BACTRLTOXIN.
DR      PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR      PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.

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KM Enterotoxin; Toxin; Signal; Superantigen.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-1.
FT DISULFID 120 137
FT CONFLICT 177 177 D -> N (IN REF. 2).
SQ SEQUENCE 266 AA; 30546 MW; 3A7AB59A8986853B CAC64;

Query Match 20.4%; Score 509; DB 1; Length 266;
Best Local Similarity 44.7%; Pred. No. 1.2e-26;
Matches 105; Conservative 44; Mismatches 70; Indels 16; Gaps 6;

QY 2 QDDPPPSLHSSSLVKNL-QNIFYLEDPTTHENVKSVDDLRSIDLTYNSG---PRYD 57
DB 30 QPDPPELDLHASKRFTGLTKENMKVLYDHYVASRVKSVDFLHDLTYNSDKKNLYD 89
QY 58 KLKTELKQENAMTLFEKNDIYGYEYHLYCE-----NAERSACIGVTNRGHN 110
DB 90 KVKTELLNEGAKKTKDEVVDYGSNTYVNCYFSSKDNVGVKGTGCTMGITRHEGN 149
QY 111 LEIP-KKIVYKVSIDQISLSPDIETNKKVTAQELDYKVKYLLTDNRKQDLYTNGPSYE 168
DB 150 FDNMGHQLVNLIRVYENKRNNTISFEVQTDKKSVTQAQELDKARNFLINKKNLYENFSSPYE 209
QY 169 TGYIKFIRKNESEFDFPEPPE--EFYOSKTLATYKNETLDS-NTQLEVLTLTK 220
DB 210 TGYIKFIENNNTPEWYDMPAPGDKFDQSKYLLMYNDMKTYDSKSKVLEVLTLTK 264

RESULT 7
EXKG_STAMM
ID EXKG_STAMM STANDARD; PRT; 258 AA.
AC 085382;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Enterotoxin type G precursor (SEG).
GN ENTE OR SEG OR SAV1824 OR SA1642.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879, 1280;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-FRI572;
RX MEDLINE=98298056; PubMed=9632603;
RA Munson S.H., Tremaine M.T., Bettley M.J., Welch R.A.;
RT *Identification and characterization of staphylococcal enterotoxin
RT types G and I from Staphylococcus aureus.*;
RL Infect. Immun. 66:3337-3348(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Mu50 / ATCC 700699, and N315;
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohba T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Matsutani-Ii Y., Takahashi N.K., Sawano T., Inoue R.-I., Kato C.,
RA Sekimizu K., Hiraoka H., Kubara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratazu K.;
RT *Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.*;
RL Lancet 357:1225-1240(2001).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -I- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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DR EMBL: AF084773; AAC26660.1; -
 DR EMBL: AP003363; BAB57986.1; -
 DR EMBL: AP003135; BAB42910.1; -
 DR HSSP: P01552; 1SBB.
 DR InterPro: IPR001961; Staph/strep-toxin.
 DR Pfam: PF01123; Staph-strep-toxin.1.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Enterotoxin; Toxin; Signal; Supranitigen; Complete proteome.
 FT CHAIN 1 25
 FT DISULFID 26 258 ENTEROTOXIN TYPE G.
 FT SIGNAL 116 133 BY SIMILARITY:
 SQ SEQUENCE 258 AA; 23940 MW; E2982101701D012C CRC64;

Query Match 17.8%; Score 444; DB 1; Length 258;
 Best Local Similarity 43.3%; Pred. No. 2.1e-22;
 Matches 101; Conservative 37; Mismatches 79; Indels 16; Gaps 6;

QY 2 QQQDDPSQLRRSSLYRN-----LQNIYFLYEGDVTENKVSVDQLNSHDLIYNVSGPNVD 57
 DB 26 QPDKLDELKNSDYKKNKGTGMNVMNLYTSPEVGRGVNSHQFLSHDLIFPIEKSYN 85
 QY 58 KLKTELKQEMATLEFKNDIDYGEVYHLCYCLE-----NAERSMC--IGVTNNEGNH 110
 DB 86 EVKTELENTLANNNKDKVDIGVYFYTCIIPKSPDINQNGCCMAYGGITFENSSN 145
 QY 111 LEIPKTIYVYVSIDGLOSLEFIDETNKWYTAQELDKYKRYLTDKQOYTNGPSKYEFG 170
 DB 146 -EDKLTLYVTIDNRSLGFTITTKNMVYTIQELDKYKRMHLEKRLYEPFGSAFEEG 204
 QY 171 YIKFIPKNSFWFDFEPEPE---FTQSKYIMLYKXNEFLDSMT-QIEVYLT 219
 DB 205 YIKFTEKNNNSFWFDFEPKELVPEYFYFLNITGDKNVDSKIMVEFLMT 257

RESULT 8
 PRTT_PORCI STANDARD; PRT; 868 AA.
 AC P43158;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 01-NOV-1995 (Rel. 32, Last annotation update)
 GN T101 protease/hemagglutinin prt precursor (EC 3.4.22.-).
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OX NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 53977;
 RX MEDLINE=95105001; PubMed=7806362;
 RA Madden T.E., Clark V.L., Kuramitsu H.K.;
 RT "Revised sequence of the Porphyromonas gingivalis prt cysteine
 protease/hemagglutinin gene: homology with streptococcal pyrogenic
 exotoxin B/streptococcal proteinase";
 RT Infect. Immun. 63:238-247(1995).
 CC -1- FUNCTION: APPEARS TO BE SPECIFIC FOR ARGININE-CONTAINING PEPTIDE
 BONDS. POSSESSES HEMAGGLUTININ ACTIVITY.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C10.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
 CC -----
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DR EMBL: M83096; -; NOT_ANNOTATED_CDS.
 DR MEROPS: C10.002; -
 DR InterPro: IPR000200; Peptidase_C10.
 DR InterPro: IPR001230; Prenyl-site.
 DR Pfam: PF01640; Peptidase_C10; 1.
 DR PRINTS: PRO0797; STREPTOPAIN.
 DR Hydrolase; Thiol protease; Signal; Hemagglutinin.
 FT SIGNAL 1 27
 FT PROPEP 28 27
 FT CHAIN 28 27 POTENTIAL.
 FT ACT_SITE 184 868 THIOL PROTEASE/HEMAGGLUTININ PRTT.
 FT ACT_SITE 327 184 BY SIMILARITY.
 SQ SEQUENCE 868 AA; 96444 MW; 45436FE32779323 CRC64;

Query Match 16.9%; Score 422; DB 1; Length 868;
 Best Local Similarity 39.0%; Pred. No. 3e-20;
 Matches 94; Conservative 37; Mismatches 94; Indels 16; Gaps 5;

QY 230 SKGIHYNOGNPNLTLPIYKVKPGEQSFVGOHATGVAATATQINKYHYPKGLKDY 289
 DB 156 SGPILMDGGYPTNLIHPLPS-----GQATGCVATAMGQIMHMKWPKASGEY 206
 QY 230 TYTLSSNPNYFNHPKLEFAISTROYNNNLIPTYSGRSNVQKMAISELMADYGISVD 349
 DB 207 DYYDMGTGTH-THVSGTFG---EYNSMKMKNISVIGISPEYKALSTMRDVSFVNM 261
 QY 350 DYGPSSGAGSSRVRQALKENFYNSHOINRSDF--SQMEOAIDELSONOPVYQGG 408
 DB 262 QPADGSGSTFIFERALKRETFHYKRSYIHRSLPGKEKMDIKRELAKENRYYVYAGA 321
 QY 409 KVG-GHAFVIGADGRNEYHYNMGMGVSDGFPRIDALNPSALSTGGAGFGNGYSAYV 467
 DB 322 DGSMDHAFVCDGYEPDGFHFHNMGMGMSNENFLNLTNGSLGTGAGDGGYSTDDEVYI 381
 QY 468 G 468
 DB 382 G 382

RESULT 9
 ETRYD_STAAG STANDARD; PRT; 258 AA.
 AC P20723;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 GN Enterotoxin type D precursor (SED).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=89359112; PubMed=2549000;
 RA Bayles K.W., Iandolo J.J.;
 RT "Genetic and molecular analyses of the gene encoding staphylococcal
 enterotoxin D";
 RT J. Bacteriol. 171:4799-4806(1989).
 RN [2]
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RC STRAIN-ATCC 23235;
 RX MEDLINE=97157473; PubMed=9003758;

RA Sundstroem M., Abrahamsen L., Antonsson P., Melhinde K., Mourad W.,
 RA Dohlsten M.;
 RT "The crystal structure of staphylococcal enterotoxin type D reveals
 RT z22+-mediated homodimerization.";
 RL EMBL J.15:6832-6840(1996).
 CC -1- SUBUNIT: HOMODIMER, ZINC-DEPENDENT.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; M28521; AAB06195.1; -
 CC PIR; A33953; A33953.
 CC HSSP; P13163; 15XT.
 DR InterPro: IPR001961; Staph/Strep toxin.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00277; BACTRTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Enterotoxin; Toxin; Signal; Superantigen; Zinc.
 FT SIGNAL 1 25
 FT CHAIN 26 258 ENTEROTOXIN TYPE D.
 FT METAL 212 212 ZINC.
 FT METAL 250 250 ZINC.
 FT METAL 252 252 ZINC.
 FT VARIANT 114 114 P -> A (IN STRAIN ATCC 23235).
 FT SEQUENCE 258 AA; 29746 MW; 4F7C6A28D42597FD CRC64;
 SO
 Query Match 11.8%; Score 295.5; DB 1; Length 258;
 Best Local Similarity 35.0%; Pred. No. 1.2e-12;
 Matches 79; Conservative 44; Mismatches 86; Indels 17; Gaps 9;
 QY 9 OLHR-----SLVKNQNIYFLYEGDPYTHENVKSVQDLRSHDLIYN--VSGPNYDKLK 60
 DB 36 ELHKSELSSTALNMKHSY--ADKNPIIGENKSTGQDFLENTLLYKFFDILNFEIDL 93
 QY 61 TELKQEMATLFKDNIDITGYEYHLCYLCENMRSC-IGVTNRGNNLEIPKTIYV 119
 DB 94 INFNRKEMAHKRSKNVYPIRSINCYGE-IDRTACTYGGVTPHEGNLKERKKLP 152
 QY 120 KVSIDGID-SLSFD-IETNNKMWTAQOELDYKVRKYLTKNKLTYNGP--SKYETGYIKFI 175
 DB 153 NWMINGVQKEVSLDKVQTDKKNVYQELDAQARRLQDKLTKNNIDTIGKGIQRKLEFD 212
 QY 176 PNKSEFMEFPEPEFTQSKLYMTKNETLDS-NTQIEVYLTGK 220
 DB 213 SSDGSVSYDLFDVAGDPEKQLRIYSNKKTLSTELHIDILYLER 258
 RESULT 10
 EXTRA STAAW STANDARD: PRT; 257 AA.
 ID ETKA STAAW
 AC P13163;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Enterotoxin type A precursor (SEA).
 GN ENTA OR MM1889.
 OS Staphylococcus aureus (strain MW2), and
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OK NCBI_TaxID=196620, 1280;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-MW2.
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA.";
 RL Lancet 359:1819-1827(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PR137;
 RX MEDLINE=88086892; PubMed=3335483;
 RA Bettle M.J., Mekalanos J.J.;
 RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
 RL J. Bacteriol. 170:34-41(1988).
 RN [3]
 RP SEQUENCE OF 25-257.
 RX MEDLINE=87222293; PubMed=3584106;
 RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
 RT "Complete amino acid sequence of staphylococcal enterotoxin A.";
 RL J. Biol. Chem. 262:7006-7013(1987).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=95354648; PubMed=7628431;
 RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohlsten M., Kalland T.,
 RA Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
 RT "Crystal structure of the superantigen staphylococcal enterotoxin
 RT type A.";
 RL EMBL J. 14:3292-3301(1995).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=97113025; PubMed=8943278;
 RA Sundstroem M., Hallen D., Svensson A., Schad E., Dohlsten M.,
 RA Abrahamsen L.;
 RT "The Co-crystal structure of staphylococcal enterotoxin type A with
 RT z22+ at 2.7-A resolution. Implications for major histocompatibility
 RT complex class II binding.";
 RL J. Biol. Chem. 271:32212-32216(1996).
 RN [6]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 RT enterotoxins.";
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN [7]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=97334373; PubMed=9191070;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 RT enterotoxins A and C2 reveals remarkable similarity and
 RT dissimilarity.";
 RL J. Mol. Biol. 269:270-280(1997).
 CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 CC for the toxin interaction with MHC class II.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; AP004828; BAB95754.1; -

DR EMBL: M18970; AAA26681.1; -
 DR PIR: A28664; A28664.
 DR PIR: A28664; A28664.
 DR PDB: 1SEF; 11-JUL-96.
 DR PDB: 1SEA; 15-OCT-95.
 DR PDB: 1SXT; 19-NOV-97.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_Strep_toxin_1.
 DR Pfam: PF02876; Staph_Strep_toxin_2.
 DR PRINTS: PR00279; BACTR1TOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2.
 DR Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 257 ENTEROTOXIN TYPE A.
 FT DISULFID 120 130
 FT METAL 211 211 ZINC.
 FT METAL 249 249 ZINC.
 FT METAL 251 251 ZINC.
 FT CONFLICT 242 242 T -> S (IN REF. 3).
 SQ SEQUENCE 257 AA; 29669 MW; ADEBF5CALF14677 CRC64;

Query Match 10.3%; Score 257.5; DB 1; Length 257;
 Best Local Similarity 31.7%; Pred. No. 3.6e-10;
 Matches 70; Conservative 44; Mismatches 94; Indels 13; Gaps 8;

QY 8 SGLHRSVLYKNLQNIIFYLEGDPVTHENKSVQDLRSHDLIN--VSGPNIDKLTLEK 64
 DB 40 SELQGNAL-GNLKQIY--YNEKAKTENKESHQDLQHTLLEFGFTDHSWYDLDVDFD 96
 QY 65 NOEMATLFRKNDIDYGEVYHLCYCEAERSACI--GGVTNEGSHLEIPKRIYKVS 123
 DB 97 SKDIYKYGKAVDLYGAYGYOC--AGGPNKTCACYGVTLLDNKRLTEKKVPINLWI 155
 QY 124 DGIQSL--SEDIETNKKWTAQELDYKVRKYLTDNQLYTN--PSKYETGYIKFIPK 179
 DB 156 DGRQNTVPLEYTKNKVTVQELDQARRYLQEKYNLNSDVFQDKVQGLIVFHTSTE 215
 QY 180 ESFMFDFPEPPEFTOSKYLMIYKDNETLDS--NTQIEVLYLT 219
 DB 216 PSVNYDLFGAQGYSTNLLRIYRDNTINSENMHIDLYLT 256

RESULT 11

ETXE_STPAU STANDARD; PRT; 257 AA.
 AC P12993;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Enterotoxin type E precursor (SEE).
 GN ENTE.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
 RC STRAIN-M0B265;
 RX MEDLINE=88257005; PubMed=3384800;
 RA Couch J.L., Solits M.T., Betley M.J.;
 RT Cloning and nucleotide sequence of the type E staphylococcal
 RT enterotoxin gene.*;
 RL J. Bacteriol. 170:2954-2960(1988).
 RN [2]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F., Jr., Pletcher J., Sax M.;
 RT Residues defining V beta specificity in staphylococcal
 RT enterotoxins.*;
 RL Nat. Struct. Biol. 2:680-686(1995).
 CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 for the toxin interaction with MHC class II (By similarity).

CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
 CC FAMILY.

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DR EMBL: M21319; AAA26617.1; -
 DR PIR: A28179; A28179.
 DR PDB: 1SEF; 15-OCT-95.
 DR InterPro: IPR001961; Staph/Strep_toxin.
 DR Pfam: PF01123; Staph_Strep_toxin_1.
 DR Pfam: PF02876; Staph_Strep_toxin_2.
 DR PRINTS: PR00279; BACTR1TOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2.
 DR Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
 3D-structure.
 FT SIGNAL 1 27
 FT CHAIN 28 257 ENTEROTOXIN TYPE E.
 FT METAL 211 211 ZINC (BY SIMILARITY).
 FT METAL 249 249 ZINC (BY SIMILARITY).
 FT METAL 251 251 ZINC (BY SIMILARITY).
 SQ SEQUENCE 257 AA; 29358 MW; 27EDA94B97770CE3 CRC64;

Query Match 10.3%; Score 256.5; DB 1; Length 257;
 Best Local Similarity 33.8%; Pred. No. 4.2e-10;
 Matches 76; Conservative 43; Mismatches 85; Indels 21; Gaps 12;

QY 8 SGLHRSVLYKNLQNIIFYLEGDPVTHENKSVQDLRSHDLIN--VSGPNIDKLTLEK 64
 DB 40 SELQGNAL-SNLKQIY--YNEKAIT--ENESDQPLENTLLFEGFTGHWYDLDVDFD 96
 QY 65 NOEMATLFRKNDIDYGEVYHLCYCEAERSACI--GGVTNEGSHLEIPKRIYKVS 123
 DB 97 SKDATNKKYKGVKVDLYGAYGYOC--AGGPNKTCACYGVTLLDNKRLTEKKVPINLWI 155
 QY 124 DGIQSL--SEDIETNKKWTAQELDYKVRKYLTDNQLYTN--PSKYETGYIKFIPK 179
 DB 156 DGRQNTVPLEYTKNKVTVQELDQARRYLQEKYNLNSDVFQDKVQGLIVFHTSTE 215
 QY 180 ESFMFDFPEPPEFTOSKYLMIYKDNETLDS--NTQIEVLYLT 219
 DB 216 STVSYDLF---AQGYPTLRIYRDNTINSENMHIDLYLT 256

RESULT 12

SPHE_STRPY STANDARD; PRT; 236 AA.
 AC Q9X5C8;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Exotoxin type H precursor (SPE H).
 GN SPEH OR SPY1008.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-M15;
 RX MEDLINE=99093428; PubMed=9874566;
 RA Proft T., Mofatt S.L., Berkahn C.J., Fraser J.D.;
 RT Identification and characterization of novel superantigens from
 RT Streptococcus pyogenes.*;

```

RL J. Exp. Med. 189:89-102(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SF370 / ATCC 700294 / Serotype M1;
RA MEDLINE-21192684; PubMed-11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RA "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RA Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -1 SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain.
CC -1 SUBCELLULAR LOCATION: Secreted.
CC -1 DISEASE: Mitogenic for human peripheral blood lymphocytes.
CC -1 SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC -----
DR EMBL: AF124500; AAD30989.1; -
DR EMBL: AE006546; AKK33907.1; -
DR HSSP: P13163; 1SXT.
DR InterPro: IPR001961; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_toxin; 1.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Signal; Complete proteome.
FT SIGNAL 1 32
FT CHAIN 33 236 EXOTOXIN TYPE H.
FT SEQUENCE 236 AA; 27485 MW; 16352923907AD40D CRC64;
SO
Query Match 8.1%; Score 203.5; DB 1; Length 236;
Best Local Similarity 32.7%; Pred. No. 1,le-06;
Matches 67; Conservative 29; Mismatches 90; Indels 19; Gaps 10;
QY 18 NLQNIYFLYEGDP--VTHENVK-SVDQLRSHDLIYNVSGPYDKLTKELKNQENATLFKD 74
DB 39 NRHMLSELYKHDSDMLIEDSIKNSPDIVTSHMLKYSVDKN---LSVFEKDWISQERKQ 95
QY 75 KNIDYGEYHYHLCYLGEMNRSACIGV--TNEGNIHLERPKTIYKVSIDGQSLSFD 132
DB 96 KEVDIYLSAQVECE-CP-GKRYAFPGITLTNSEKKEIKVP---VNVMDKSKQPPMF 149
QY 133 IETNKKMVTYQOELDYKAKYLTDNKQLYTNGSPYETGYIKFIPKNKESPFED--FPPEP 190
DB 150 ITVKKPVTYQOEVQIDIKRKLIRKYDIYNNREQKYSKGYITLDLNSGRDIYFDLYTGNG 209
QY 191 EFTOSKTLMIYKKNETLDSNTQIEV 215
DB 210 DF--NSMLKIYSNNERIDS--TOFHY 231

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RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-52.
RC STRAIN-T18P / MGAS 1585;
RA MEDLINE-88314303; PubMed-3045005;
RA Goshorn S.C., Schlievert P.M.;
RA "Nucleotide sequence of streptococcal pyrogenic exotoxin type C.";
RA Infect. Immun. 56:2518-2520(1988).
RN [2]
RP REVISIONS TO 21-26.
RC STRAIN-T18P / MGAS 1585;
RA MEDLINE-92363541; PubMed-1500157;
RA Kapur V., Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RA "Molecular population genetic evidence of horizontal spread of two
RA alleles of the pyrogenic exotoxin C gene (speC) among pathogenic
RA clones of Streptococcus pyogenes.";
RA Infect. Immun. 60:3513-3517(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-SF370 / ATCC 700294 / Serotype M1;
RA MEDLINE-21192684; PubMed-11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RA "Complete genome sequence of an M1 strain of Streptococcus
RA pyogenes.";
RA Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-235.
RA MEDLINE-97397352; PubMed-9253413;
RA Rousset A., Anderson B.F., Baker H.M., Fraser J.D., Baker E.N.;
RA "Crystal structure of the streptococcal superantigen Spe-C:
RA dimerization and zinc binding suggest a novel mode of interaction
RA with MHC class II molecules.";
RA Nat. Struct. Biol. 4:635-643(1997).
RN -1 SUBUNIT: Binds to major histocompatibility complex class II beta
RN chain.
RN -1 DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
RN THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
RN FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
RN DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
RN FEVER.
RN -1 MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
RN -1 SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
RN FAMILY.
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RN -----
DR EMBL: M35514; AAA27017.1; ALT_SEQ.
DR EMBL: M97156; AAB59091.1; -
DR EMBL: M97157; AAB59092.1; -
DR EMBL: AE006523; AKK33664.1; -
DR PIR: A30509; A30509.
DR PDB: 1AN8; 29-APR-98.
DR InterPro: IPR001961; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Toxin; Signal; 3D-structure; Complete proteome.
FT SIGNAL 1 27
FT CHAIN 28 235 EXOTOXIN TYPE C.
FT CONFLICT 53 53 N -> D (IN REF. 1).
FT SEQUENCE 235 AA; 27371 MW; 070534AAB952C1E0 CRC64;
SO
Query Match 7.3%; Score 183; DB 1; Length 235;

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DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE: PS00277: STAPH STREP TOXIN 1. EAISE NEG

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CC -----

DR EMBL: X70039: CAA9633.1; -

DR EMBL: AF282853: AAC44706.1; -

DR InterPro: IPR005169: Caga.

DR Pfam: PF03507: Caga.1.

DR PRINTS: PR01553: TYPEASSCAGA.

KM Antigen.

FT DOMAIN

FT CONFLICT

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Query Match 4.9% Score 123; DB 1; Length 1147;

Best Local Similarity 19.4%; Pred. No. 1.8; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

Matches 120; Conservative 97; Mismatches 184; Indels 218; Gaps 29;

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Search completed: June 23, 2003, 16:13:02
Job time : 20.2253 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

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Run on:      June 23, 2003, 16:10:06 ; Search time 34.4979 Seconds
              (Without alignments)
              1304.163 Million cell updates/sec
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Title: US-10-002-784A-27
 Page: 3500

Sequence: 1 MQQDPDPSQLHRSSLVKNLQ.....ALGTGGGAGGFNGYQSAVVG 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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post-processing:	Minimum Match	0%
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Listing first 45 summaries

Database :

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PIR_73:*
1: plr1:*
2: plr2:*
3: plr3:*
4: plr4:*
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Pred. No. Is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1327.5	53.1	398	2	A37768	streptococcal pyruvate
2	1198	47.9	337	1	BSP0	streptopain (EC 3.4.21.1)
3	1129	45.2	251	1	S29659	exotoxin type A protein
4	1096.5	43.9	236	2	S18783	exotoxin type A protein
5	1089.5	43.6	236	2	S18786	exotoxin type A protein
6	986.5	39.5	236	2	S18789	exotoxin A precursor
7	938.5	37.5	250	1	A26152	streptococcal pyruvate
8	541	21.6	266	1	ENSAB6	enterotoxin B precursor
9	513	20.5	266	1	S11885	enterotoxin C3 - 5
10	510	20.4	266	2	A60114	enterotoxin C-2 protein
11	509	20.4	266	2	ENSAC1	extracellular enterotoxin
12	444	17.8	258	1	G89968	cyteine proteinase
13	422	16.9	866	2	T10890	enterotoxin D precursor
14	303.5	12.1	136	2	A89969	enterotoxin D precursor
15	295.5	11.8	258	2	A33553	enterotoxin D precursor
16	291.5	11.7	260	2	E89969	enterotoxin D precursor
17	279.5	10.5	260	2	G89984	enterotoxin D precursor
18	263	10.5	240	2	G89991	enterotoxin D precursor
19	262.5	10.5	258	2	H89968	enterotoxin D precursor
20	257.5	10.3	257	2	A28664	enterotoxin D precursor
21	256.5	10.3	257	2	A28179	enterotoxin D precursor
22	237.5	9.5	239	2	D89969	enterotoxin D precursor
23	218	8.7	242	2	C89969	enterotoxin D precursor
24	183	7.3	235	2	A30509	enterotoxin D precursor
25	173	6.9	133	2	B89969	enterotoxin D precursor
26	154.5	6.2	855	2	H82885	hypothetical protein
27	137	5.5	250	2	G71609	hypothetical protein
28	132.5	5.3	231	2	D89807	hypothetical protein
29	124.5	5.0	750	2	G81361	probable flagellin

30	124.5	5.0	1183	2	F90559	conserved hypother
31	123.5	4.9	616	2	G82885	hypothetical protei
32	123	4.9	227	2	C85808	exotoxin 15 (impor
33	123	4.9	1315	2	B48281	cytochrome-associa
34	122.5	4.9	960	2	S72284	DNA-directed RNA p
35	122.5	4.9	1146	2	A89922	conserved hypother
36	121	4.8	1881	2	H95076	zinc metalloprotei
37	120.5	4.8	378	2	AD1541	hypothetical protea
38	120.5	4.8	2401	2	T28676	riophery protein -
39	119	4.8	351	2	D89991	hypothetical prote
40	118	4.7	1306	2	T25313	ORF MSV152 probabl
41	117	4.7	675	2	S16624	penicillin-binding
42	117	4.7	1886	2	C64588	ceg pathogenicity
43	116.5	4.7	770	2	B48910	desmocollin 1b pre
44	116.5	4.7	824	2	A48910	desmocollin 1a pre
45	116.5	4.7	840	2	I37281	Dactin precursor -

ALIGNMENTS

RESULT 1
 A37768
 Streptococcal pyrogenic exotoxin type B precursor - Streptococcus pyogenes
 C:Species: Streptococcus pyogenes
 C:Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 22-Jun-1999
 C:Accession: A37768
 R:Hauser, A.R.; Schlievert, P.M.
 J. Bacteriol. 172, 4536-4542, 1990
 A:Title: Nucleotide sequence of the streptococcal pyrogenic exotoxin type B gene and
 A:Reference number: A37768; MUID:90330563; PMID:2198264
 A:Accession: A37768
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-398 <HAU>
 A:Cross-references: GB:M66905; GB:M35110; NID:g153818; PIDD:AAA26938.1; PID:g153819
 C:Superfamily: streptococcal cysteine proteinase
 C:Keywords: exotoxin

Query Match	Score	DB 2;	Length
Best Local Similarity	53.18;	1327.5;	398
Best Local Similarity	61.59;	146.20;	

Matches	258;	Conservative	5;	Mismatches	8;	Indels	11;	Gaps	5;
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192 FTQSKYLMYKDNETLDSNTQIEVYLT --KOPVVKSLDSDSGIHYNOCNPYNLLTPVI 248

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120 FMES-YVEOIKENKKI.DT-----TYAGTAETKOPVXSI.DSKCIHYNOCNBYNI.TEYVI 173

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309 AISTKQINWNNILPTYSGR:SNVQKMAISELMADVGISVDMIDYGPSSGCSAGSSRVQRAIK 368

234 AISTRÖYNWNNILPTYSGRESNVQKMAISELMADVGISVDMGYGPSSGSAGSSRVQALK 293

369 ENFGYNQSVHQINRSDFS-QDWEAQIDKELSQNOPYYQG-GKVGCHAFVIDGADGRNFY 426

294 ENFGYNQSVHQINRSDFSKQDWEAQIDKELSQNQPPVYYQGVGVGHAFVIDGADGRNEY 353

427 HVNWGCGVSDGEFFRLDALNP^{SA}LGTTGGAGGFGNGY^{SA}AVG 468

354 HVNMGVSGVSDGEFRI.DAI.NPSAIGTGGGAGCENCYOSAYYC 395

RESULT 2

Streptopain (EC 3.4.22.10) precursor - Streptococcus pyogenes

Alternate names: streptococcal cysteine proteinase; streptococcal peptidase A
Species: *Streptococcus pyogenes*

Date: 24-Apr-1984 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
Accession: S076669.100078

Yonahba, K.; Elliott, S.D.; Liu, T.Y.

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M.Alternate names: scarlet fever toxin
C.Species: Streptococcus pyogenes phage
A.Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strai
Isolate United Kingdom; strain MGAS496 isolate Germany
C.Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #tent_change 16-Jul-1999
C.Accession: S18786; S18787; S18788; S18790; S18792; S18795; S18799
R.Nelson, K.; Schlievert, P.M.; Selander, R.R.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A.Title: Characterization and clonal distribution of four alleles of the speA gene en
A.Reference number: S18782; MUID:92044323; PMID:1940804
A.Accession: S18786
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61561; NID:q47297; PIDN:CAA43759.1; PID:q47298
A:Experimental source: strain MGAS250 isolate California unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1999
A:Accession: S18787
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61562; NID:q47299; PIDN:CAA43760.1; PID:q47300
A:Experimental source: strain MGAS251 isolate California unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1999
A:Accession: S18788
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61563; NID:q47301; PIDN:CAA43761.1; PID:q47302
A:Experimental source: strain MGAS256 isolate California unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1999
A:Accession: S18790
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61564; NID:q47305; PIDN:CAA43762.1; PID:q47306
A:Experimental source: strain MGAS285 isolate Colorado unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1999
A:Accession: S18792
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61565; NID:q47311; PIDN:CAA43763.1; PID:q47312
A:Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1999
A:Accession: S18795
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEU>
A:Cross-references: EMBL:X61566; NID:q47317; PIDN:CAA43764.1; PID:q47318
A:Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1999
A:Accession: S18799
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NES>
A:Cross-references: EMBL:X61567; NID:q47325; PIDN:CAA43765.1; PID:q47326
A:Experimental source: strain MGAS496 isolate Germany unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1999
C.Genetics:
A:Gene: speA2
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F.I-22/Domin: signal sequence (fragment) #status predicted <SIG>
F.I-23/Product: exotoxin type A (fragment) #status predicted <MAT>
Query Match      43.6% Score 1089.5 DB 2: Length 236;
Best Local Similarity 97.6%; Pred No. 2.7e-64;
Matches 206; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

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QY 62 LKKNQEWATLEFKNDINIDYGEYHYHLCYLEENRERACI -GGVYNREGNHLIEPKKIYVK 120
 DB 83 ELKKNQEWATLEFKDNVDIYSVEYHYHLCYLEENRERACIIGGVYNREGNHLIEPKKIYVK 142
 QY 121 VSIDGIQSLSPDIEFNKKMWTAAQELDYKVRKYLTDNKKQLYTNGSPSKYETGYIKFIPKNKE 180
 DB 143 VSIDGIQSLSPDIEFNKKMWTAAQELDYKVRKYLTDNKKQLYTNGSPSKYETGYIKFIPKNKE 202
 QY 181 SFWDFPFPEPEFTQSKYLMYIKDNETLDSNT 211
 DB 203 SFWDFPFPEPEFTQSKYLMYIKDNETLDSNT 233
 RESULT 6
 S18789
 N:Alternate names: scarlet fever toxin
 C:Species: Streptococcus pyogenes
 A:Variety: strain MGAS262 isolate California
 C:date: 29-Jan-1999 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
 C:Accession: S18789
 R:Nelson, K.; Schlievert, P.M.; Seldander, R.K.; Musser, J.M.
 J. Exp. Med. 174, 1271-1274, 1991
 A:Title: Characterization and clonal distribution of four alleles of the speA gene encoded
 A:Reference number: S18782; MUID:92044323; PMID:1940804
 A:Accession: S18789
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-236 <NEU>
 A:Cross-references: EMBL:X61573; NID:947303; PIDN:CAA3771.1; PID:947304
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 C:Genetics:
 A:Gene: speA
 C:Superfamily: enterotoxin B
 C:Keywords: exotoxin
 F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
 F:23-236/Product: exotoxin A (fragment) #status predicted <MAT>
 Query Match 39.5%; Score 986.5; DB 2; Length 236;
 Best Local Similarity 88.2%; Pred. No. 1.5e-57;
 Matches 186; Conservative 13; Mismatches 11; Indels 1; Gaps 1;
 QY 2 QDDPDPQSLHRSSLYKNLQNTYFLYEGDPVTHENKVSVDLSHDLIYNVSGPNYDKLT 61
 DB 23 QDDPDPQSLHRSSLYKNLQNTYFLYEGDPVTHENKVSVDLSHDLIYNVSGPNYDKLT 82
 QY 62 ELKKNQEWATLEFKDNVDIYGEYHYHLCYLEENRERACI -GGVYNREGNHLIEPKKIYVK 120
 DB 83 ELKKNQEWATLEFKDNVDIYGEYHYHLCYLEENRERACIIGGVYNREGNHLIEPKKIYVK 142
 QY 121 VSIDGIQSLSPDIEFNKKMWTAAQELDYKVRKYLTDNKKQLYTNGSPSKYETGYIKFIPKNKE 180
 DB 143 VSIDGIQSLSPDIEFNKKMWTAAQELDYKVRKYLTDNKKQLYTNGSPSKYETGYIKFIPKNKE 202
 QY 181 SFWDFPFPEPEFTQSKYLMYIKDNETLDSNT 211
 DB 203 SFWDFPFPEPEFTQSKYLMYIKDNETLDSNT 233
 RESULT 7
 A26152
 streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
 N:Alternate names: scarlet fever toxin; SPE type A (speA)
 C:Species: Streptococcus sp.
 C:date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A26152
 R:Johnson, L.P.; L'Italian, J.J.; Schlievert, P.M.
 Mol. Gen. Genet. 203, 354-356, 1986
 A:Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Staphylococcus aureus exotoxin A
 A:Reference number: A26152; MUID:86584313; PMID:3526093
 A:Accession: A26152
 A:Molecule type: DNA

A:Residues: 1-250 <JOH>
C:Superfamily: enterotoxin B
C:Keywords: exotoxin

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Query Match          37.5%   Score 938.5; DB 1; Length 250;
Best Local Similarity 84.9%   Pred. No. 2,3e-54;
Matches 185; Conservative 5; Mismatches 25; Indels 3; Gaps 3;
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Oy PDPSQLRRSSLYVKMLQNIYFLEYEDPDPTHTENKSVSDQLRSHDLITVNVSGPNYLKTLELK 64
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db PKPQDQRSLNLYTKFKKIYIFPMRTVLTHENVKSVDQLLSHDLLIVNSGPNYDKLTLELK 93

Oy MOENATLFKKDNIDIVGEVYYHLICYLCENAKRSACI-GGYTNREGNHLEIPKKIYAVKSI 123
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db NOEMATLFKKDNVIDYGEVYYHLICYLCENAKRSACILGGVTNHEGNHLEIPKKIYAVKSI 153

Oy DGIQSLSFDIEETNNKNNTAQLGDYKVRKYTLTDNKQLTNPSPSYETGYIKFIKRNKESEFW 183
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db DGIQSLSLDIEIQIN-GNCSTRISTYKRVKLTDNKQLTNPSPSKETGYIKFIKRNKESEFW 212

Oy 184 FDFPEPEFTQSKYLMITYKDNETLDSNT-QIEVYLTRYK 220
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 213 FDFPEPEFTQSKYLMITYKDNETLDSNTQIEVYLTRYK 250

RESULT 8
ENSAB6
enterotoxin B precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 24-Apr-1984 #sequence.revision 15-Oct-1996 #text_change 18-Jun-1999
C:Accession: S27360; A92065; S27240; A01815
R:Jones, C.L.; Khan, S.A.
J. Bacteriol. 166, 29-33, 1986
A>Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.
A:Reference number: S27360; MUID:86168029; PMID:3957869
A:Accession: S27360
A:Molecule type: DNA
A:Residues: 1-266 <JON>
A:CROSS-references: EMBL:M11118; NID:g152999; PIDD:NAA88550.1; PID:g153000
A:Experimental source: strain S6
R:Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3518-3525, 1970
A>Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen brot
A:Reference number: A92065; MUID:71007902; PMID:5470821
A:Accession: A92065
A:Molecule type: protein
A:Residues: 28-55, NMD, 59-68, 'NE', 71, 'FDLIYL', 78-117, 119-127, 'N', 129, 'D', 131-132, 'EN
A:Experimental source: strain S-6
R:Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3511-3517, 1970
A>Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, compos
A:Reference number: A92064; MUID:71007901; PMID:5470820
A:Contents: annotation; chymotryptic peptides
R:Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3493-3510, 1970
A>Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, compos
A:Reference number: A92063; MUID:71007900; PMID:5470819
A:Contents: annotation; tryptic peptides
R:Schantz, E.J.; Reesler, W.G.; Wegman, J.; Spero, L.; Dunmery, D.A.; Bergdoll, M.S.
Biochemistry 4, 1011-1016, 1965
A>Title: Purification of staphylococcal enterotoxin B.
A:Contents: annotation; A90548; MUID:66035792; PMID:44953912
R:Alakhov, V.Y.; Klinksy, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Svess
Eur. J. Biochem. 209, 823-828, 1992
A>Title: Identification of functionally active fragments of staphylococcal enterotoxin
A:Reference number: S27240; MUID:93049338; PMID:14425690
A:Accession: S27240
A:Molecule type: protein
A:Residues: 28-42, 128-148 <ALA>
C:Superfamily: enterotoxin B
C:Keywords: enterotoxin; extracellular protein; toxin
E1-27/Domains: signal sequence *status predicted <SIG>

C:Species: Staphylococcus aureus

C;Species: Staphylococcus aureus
C;Date: 09-Mar-1990 #accu0000 22

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#sequence_revision 09-Mar-1990 #text_change 15-Oct-1999
C:Accession: A33953

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R; Bayles, K.W.; Iandolo, J.J.
J. Bacteriol 171: 4799-4905

J. Bacteriol. 171, 4799-4806, 1989

A1;Reference number: A33953; MUID:89359112; PMID:2549000
A2;Accession: A33053
A3;Reference: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin A

A;Status: preliminary

A: molecule type: DNA

A: C:\PROG~1\OFFICE\EXCEL\BAY

C:Superfamily: enterotoxin B
 Cross references: GB:M2852L; NID:g1492109; PIDN:AB06195.1; PID:g758691

[illegible]

Query Match	11.8%	Score 295.5	DB 2	Length 258
Query Match	11.8%	Score 295.5	DB 2	Length 258

Best Local
Matchbook 7

11.8%; Score 295.5; DB 2; Length 258;
35.0%; Pred. No. 3.3e-12;

matches	79;	conservative	44;	Mismatches	86;	Indels	17;	Gaps	9;
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[illegible]

D6 36 EHHKSELSTALNNMKHSY--ADKNPIIGENKSGDQFLENTLTIYKFFETDINFE¹DL¹ 93

61 TELKNOENATLFFKDKNIDYGV EYHLCYL CENASAC -IGV TNREGNHL EIPKIV 119

Db 94 INFNSKEMAQHFSSKNVDVYPPIRSINCYGGE-IDRTACTYGGVTPPEHGKCLKERRKPIPI 152

QY 120 KVSIDIGQ-SLSFD-IETNKKMYIAOELDYKRYKLYTDNKOLYNGP-SKYETGYIKFI 175

Db
153 NLWINGVQKEVSLDKVQTDKKNVTVQELDAQARRYLQKDLKLYNNDTLGSKIQSGKTEFD 212

176 PKNKSEFWDEFFPEPEFTQSKYLMYKDNELDS-NTQIEVYL7TK 220

213 SSDGSKVSYDLFDVKGDPPEKQLRISDNKTLSTEHLLHIDIIYLYEK 258

Search completed: June 23, 2003, 16:15:55
Job time : 35.4979 secs

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